

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: August 10, 2004, 13:51:42 ; Search time 1294 seconds
(without alignments)
Title: US-09-875-228-1_COPY_5976_9620
Perfect score: 3645
Sequence: 1 ggccctcaataatgttaäg.....ggaggaggctgtggactggc 3645
Scoring table: Oligo_NUC
Gapop=60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 150

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

Database :	N_Geneseq_29Jan04:*
	1: geneseqn1980:*
	2: geneseqm1990s:*
	3: geneseqn2000s:*
	4: geneseqn2010as:*
	5: geneseqm2001bs:*
	6: geneseqm2002bs:*
	7: geneseqn2003as:*
	8: geneseqm2003bs:*
	9: geneseqm2003cs:*
	10: geneseqn2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	3645	100.0	12047	2	AAV17618	Homo sapi
2	3645	100.0	12047	2	AAZ06489	Human gla
3	3645	100.0	12047	3	AAZ99834	DNA, sequ
4	3645	100.0	12047	5	AAT16852	Nucleotid
5	3645	100.0	12047	5	AAH43617	Human gla
6	3645	100.0	12047	5	AAF87248	Human gla
7	3645	100.0	12047	6	ABK99584	Mucin tra
8	3645	100.0	12047	7	ACD07307	Human gla
9	3400	93.3	12047	2	AAX24755	Human gla
10	1172	32.2	1172	2	AAX24772	Human gla
11	1172	32.2	1172	2	AAZ06494	hKLK2 enh
12	1114	30.6	1558	3	AAZ94285	Human pro
13	993	27.2	1172	2	AAX24774	Human gla
14	993	27.2	1172	2	AAX24773	Human gla
15	993	27.2	1172	2	AAZ06495	hKLK2 enh
16	993	27.2	1172	2	AAX06496	hKLK2 enh
17	204	5.6	204	5	AAF82694	Glandular

ALIGNMENTS

Query Match Score 3645; DB 2; Length 12047;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ 1 GGCCCTCAATAATTGTTAAGAGTGTAAATGNGTCAAAAGATGGAAATGTTGAGACTA 60

QY	2221	CATATTGTTATTATGTCCTGAAACAGTAAACAATCTGTGAAAATAGACGTTAAGCTT	2280	QY	3301	CCTGGTGTCCGATAAGATCCTAGAACCGAAACAGGACTAAAGGTGCTAGAGAA	3360					
Db	8196	CATATTGTTATTATGTCCTGAAACAGTAAACAATCTGTGAAAATAGACGTTAAGCTT	8255	Db	9276	CCTGGTGTCCATAAGATCCTAGAACCGAAACAGGACTAAAGGTGCTAGAGAA	9335					
QY	2281	ATTATCTAAGCTAGGAAACCTAGATCTGAGGCATAACCATCTGTCAAGGCTATCT	2340	QY	3361	TGGCCATATGTCGTGTCCTCCATGAAATCTCAAGGACTTCCTGGTGAAGGCCACAGGAGCT	3420					
Db	8256	ATTATCTAAGCTAGGAAACCTAGATCTGAGGCATAACCATCTGTCAAGGCTATCT	8315	Db	9336	TGGCCATATGTCGTGTCCTCCATGAAATCTCAAGGAGCTTCCTGGTGAAGGCCACAGGAGCT	9395					
QY	2341	GCTGTACAAATAATGTTGAAAGATGGTCCAGAAAAGAAAACCGTATATTGCTTCT	2400	QY	3421	GAACATACGGGTTGCCCTGTCCTGTCCTGCAAGCAGTCAGTCAGTCAGTCAGGCA	3480					
Db	8316	GCTGTACAAATAATGTTGAAAGATGGTCCAGAAAAGAAAACCGTATATTGCTTCT	8375	Db	9396	GAACATACGGGTTGCCCTGTCCTGTCCTGCAAGCAGTCAGTCAGTCAGTCAGGCA	9455					
QY	2401	CAGAGACACAGACAGAAACATAAGAGAACTGGAAAATGTCTCCACACTGTCAACC	2460	QY	3481	CTGTGCGAGCATGTCGTTCATCTGACCAATCTGTAAAGGGCTTACCCAGGACCCCTG	3540					
Db	8376	CAGAGACACAGACAGAAACATAAGAGAACTGGAAAATGTCTCCACACTGTCAACC	8435	Db	9456	CTGTGCGAGCATGTCGTTCATCTGACCAATCTGTAAAGGGCTTACCCAGGACCCCTG	9515					
QY	2461	AGAGGCTTCACCTCTGTCAGGACAGCTTAAACATCCATCATTAAGTGTTCTACCA	2520	QY	3541	ATGAACACCATGTTGTCAGGACAGAGGGGTGAGGGCATGGATTCCTCTGTGTCAA	3600					
Db	8436	AGAGGCTTCACCTCTGTCAGGACAGCTTAAACATCCATCATTAAGTGTTCTACCA	8495	Db	9516	ATGAACACCATGTTGTCAGGACAGAGGGGTGAGGGCATGGATTCCTCTGTGTCAA	9575					
QY	2521	CATCGGCTTACCGTCCCTAACGAGTTCTAGGTCCAGTTCCACCACTTTCGA	2580	QY	3601	GCCCCAGGGGCCATGACGGTCTGGGGCTGGGGCTGGACTGGCTGG	3645					
Db	8496	CATCGGCTTACCGTCCCTAACGAGTTCTAGGTCCAGTTCCACCACTTTCGA	8555	Db	9576	GCCCCAGGGGCCATGACGGTCTGGGGCTGGGGCTGGACTGGCTGG	9620					
QY	2581	GTGCCCTACGTGCCAACCCCGAAATAGAGACATGGGGACATGGTGG	2640	RESULT 2								
Db	8556	GTGCCCTACGTGCCAACCCCGAAATAGAGACATGGGGACATGGGG	8615	ID	AAZ06489	standard; DNA: 12047 BP.						
QY	2641	GGATGAAACTTCTGGCTGAGTGCAGAGGGGCCAACTCTTGGTCTCAAGGG	2700	XX	AAZ06489;							
Db	8616	GGATGAAACTTCTGGCTGAGTGCAGAGGGGCCAACTCTTGGTCTCAAGGG	8675	XX	DT	23-NOV-1999 (first entry)						
QY	2701	AAGAGGCTGGAGGTCAAATGTCCTGAAAGGGGAAATGGGGTCTGAACCTTAATCC	2760	XX	DE	Human glandular kallikrein-1 (hGK1/hhKLK2) promoter/enhancer region.						
Db	8676	AAGAGGCTGGAGGTCAAATGTCCTGAAAGGGGAAATGGGGTCTGAACCTTAATCC	8735	XX	XX	Prostate; cancer; drug assay; drug development; enhancer; promoter; tumour; kallikrein; androgen regulation; prostate specific antigen; ss.						
QY	2761	CCAAGGGAGGAGATGTTAAAGGTCCAGTTCCGAGGAAATGGGGTCAAGTGCAG	2820	XX	XX							
Db	8736	CCAAGGGAGGAGATGTTAAAGGTCCAGTTCCGAGGAAATGGGGTCAAGTGCAG	8795	CS	Homo sapiens.							
QY	2821	AGGGCTTAAGAATCCCGTATCCTCGGGAAAGGGGCTAAATGTCGAGGGTTCAGTGC	2880	XX	XX							
Db	8796	AGGGCTTAAGAATCCCGTATCCTCGGGAAAGGGGCTAAATGTCGAGGGTTCAGTGC	8855	FT	Key Qualifiers							
QY	2881	AGGGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTT	2940	XX	enhancer	AAZ06489						
Db	8856	AGGGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTT	8915	FT	/ *tag=	a						
QY	2941	GGCTCCAGGTTTGTGTGAGGTTATGGGATCTCTGATTCTCAAGGGTCAAGGACT	3000	XX	/note= "Enhancer activity"							
Db	8916	GGCTCCAGGTTTGTGTGAGGTTATGGGATCTCTGATTCTCAAGGGTCAAGGACT	8975	XX	XX							
QY	3001	GAGAGTTGCCATGCTTGTAACTCTTCACTTCACTTCACTTCACTTCACTTCA	3060	PN	W0941413-A2.							
Db	8976	GAGAGTTGCCATGCTTGTAACTCTTCACTTCACTTCACTTCACTTCACTTCA	9035	PN	W0941413-A2.							
QY	3061	TACTCTTGTAGTTCCACAGAGTGGCTTCACTCATCTGCAATGTCATGCCATTC	3120	XX	XX							
Db	9036	TACTCTTGTAGTTCCACAGAGTGGCTTCACTCATCTGCAATGTCATGCCATTC	9095	PD	19-AUG-1999.							
QY	3121	CCGAGGCCTGGGCTATCATCATCATTCAGGATCTGGCTATGGGGCAGGCCGG	3180	XX	XX							
Db	9096	CCGAGGCCTGGGCTATCATCATCATTCAGGATCTGGCTATGGGGCAGGCCGG	9155	PP	11-FEB-1999;							
QY	3181	CCGCTATGAGCTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC	3240	XX	XX							
Db	9156	CCGCTATGAGCTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC	9215	PP	12-FEB-1999;							
QY	3241	CCATGGAGCTGGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTG	3300	PR	98US-00022732.							
Db	9216	CCATGGAGCTGGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTG	9275	XX	XX							
QY				PA	(CALY-) CALYDON INC.							
Db				PI	Henderson DR, Lamparski HG, Schutur ER, Yu DC;							
QY				XX	WPI; 1999-527378/44.							
Db				XX	Screening for compounds which inhibit prostate cancer using a cell line							
QY				PT	containing a marker whose expression is responsive to therapeutic							
Db				PT	active compounds.							
QY				XX	This is the nucleotide sequence of the promoter/enhancer region of the							
Db				XX	human glandular kallikrein gene (hGK1 or hKLK2, encoding the hK2 protein). hKLK2 is a member of the kallikrein family, as is the prostate-specific antigen (PSA), a chymotrypsin like protein that is synthesized exclusively by normal, hyperplastic, and malignant prostatic epithelia.							
QY				XX	This tissue specific nature of PSA makes it an excellent biomarker for identifying benign prostatic hyperplasia (BPH) and prostatic carcinoma (Cap). Elevated levels of PSA are indicative of BPH or Cap. Like PSA,							
Db				PS	Example 6; Page 44-48; 50pp; English.							
QY				XX	This is the nucleotide sequence of the promoter/enhancer region of the							
Db				XX	human glandular kallikrein gene (hGK1 or hKLK2, encoding the hK2 protein). hKLK2 is a member of the kallikrein family, as is the prostate-specific antigen (PSA), a chymotrypsin like protein that is synthesized exclusively by normal, hyperplastic, and malignant prostatic epithelia.							
QY				XX	This tissue specific nature of PSA makes it an excellent biomarker for identifying benign prostatic hyperplasia (BPH) and prostatic carcinoma (Cap). Elevated levels of PSA are indicative of BPH or Cap. Like PSA,							

CC hKLU2 is expressed exclusively in the prostate and is up regulated by androgens, primarily by transcription activation. The proteins also exhibit a high degree of amino acid sequence identity and contain similar regulatory elements. The characterisation of genes whose expression is limited to the prostate allows the development of screening methods which can identify substances capable of specifically altering the expression of prostate-specific genes

CC	Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other;	Qy	901 GACAAGGAGAGCTCAAGCAGATTCCAGCTTCTGGTTCCAGTGTGTCATGGAAA 960
CC	Query Match 100.0%; Score 3645; DB 2; Length 12047;	Db	6876 GACAAGGAGAGCTCAAGCAGATTCCAGTGTGTCATGGAAA 6935
CC	Best Local Similarity 100.0%; Pred. No. 0;	Qy	961 GGATATCTCTCCATACATGATGTGATAATAATCGTATTGCAATCGGGAAAC 1020
CC	Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	6936 GCAGPATCCTTCATACATGATGTGATAATAATCGTATTGCAATCGGGAAAC 6995
xx		Qy	1021 TOAATGAGCCTGATATAATTGGACTCTGGTTCACAGCATCTGCACACCTTCATGG 1080
SQ		Db	6996 TCAACTGAGCCTTGATATAATTGGAGCTGACAGACATCTGACCCCTCATCG 7055
		Qy	1081 CTGAACATTACTAGCCCTCCAAGCTTAAGCTGATACTGGTAAACCAATT 1140
		Db	7056 CTGAACTTAGACTAGCCCTCCAAGCTTAAGCTGATACTGGTAAACCAATT 7115
		Qy	1141 GTCACCCATAAATCAGCTGGTAACTATCGATGGCTCCGCAAGTGGCAACAG 1200
		Db	7116 GTCACCAATAATCATTTGATATACTTGTAGATATCGATGGCCAAAGTGGCAAG 7175
		Qy	1201 GCACCTAAACAGGGGATATTCAAAAGCTTAAAGATGATGACCTCCAGGAGCTGATGC 1260
		Db	7176 GCACCTAAACAGGGGATATTCAAAAGCTTAAAGATGACCTCCAGGAGCTGATGC 7235
		Qy	1261 AAAGACTGGCCTCTGGCAAGCAGAACTCTTACCCCAACTCTCTCACAGGTT 1320
		Db	7236 AAAGACTGGCCTCTGGCAAGCAGAACTCTTACCCCAACTCTCTCACAGGTT 7295
		Qy	1321 ATGGAGGATCAANTGGCTCATGTGTGAGCACCGCACCTGTCTGGCTGTGAGA 1380
		Db	7296 ATTGAGGATCAANTGGCTCATGTGTGAGCACCGCACCTGTCTGGCTGTGAGA 7355
		Qy	1381 GTGACTCTATGTGTGCTAACATGGTAAAGGATTTAGGATGCTCTTGTAG 1440
		Db	7356 GTGACTCTATGTGTGCTAACATGGTAAAGGATTTAGGATGCTCTTGTAG 7415
		Qy	1441 CACTCAGATGCTCATCPAATCTCACACATGGTACAGCTGGGCACTACTGGCTC 1500
		Db	7416 CACTCAGATGCTCATCPAATCTCACACATGGTACAGCTGGGCACTACTGGCTC 7475
		Qy	1501 ATTTGACAGAGGAAGGACTGTGGATAAGGGGGTGRACCAATAGGTCAAGTCATCT 1560
		Db	7476 ATTTGACAGAGGAAGGACTGTGGATAAGGGGGTGRACCAATAGGTCAAGTCATCT 7535
		Qy	1561 GGATGAAAGGGGCTCAAGGACCATTAGGACATTAGGACATTGGCAATCTGG 1620
		Db	7536 GGATGAAAGGGGCTCAAGGACCATTAGGACATTGGCAATCTGGCAATCTGG 7595
		Qy	1621 ATGTCCTGCCCCGAAGGGGGTGCATTTCCTGGCAATCTGGCAATCTGG 1680
		Db	7596 ATGTCCTGCCCCGAAGGGGGTGCATTTCCTGGCAATCTGGCAATCTGG 7655
		Qy	1681 TTGAGGTTATCTCAGACTCTCTPATGATACCCAGGCCATATACTCTGTGTC 1740
		Db	7656 TTGAGGTTATCTCAGACTCTCTPATGATACCCAGGCCATATACTCTGTGTC 7715
		Qy	1741 TCTCCCTTCTCATCTACTGCCACTCTCCAGTCCATCTGGCAATCTGG 1800
		Db	7716 TCTCCCTTCTCATCTACTGCCACTCTCCAGTCCATCTGGCAATCTGG 7775
		Qy	1801 TAGGCCAGTACCTTAATCTGAGGAGACTATAATGTTGAGGAGACTATAATGTT 1860
		Db	7776 TAGGCCAGTACCTTAATCTGAGGAGACTATAATGTTGAGGAGACTATAATGTT 7835
		Qy	1861 AAAAAAAGAAACTCTGAARGAGGTGACATTACCGGACTCTGCAACATAGCTAACT 1920
		Db	7836 AAAAAAAGAAACTCTGAARGAGGTGACATTACCGGACTCTGCAACATAGCTAACT 7895
		Qy	1921 CCAGTTTGGCTGCTGACTCATGAGGAAAGGTCATGGCTCTGGCTGAGGCAAAG 1980
		Db	7896 CCAGTTTGGCTGCTGACTCATGAGGAAAGGTCATGGCTCTGGCTGAGGCAAAG 7955
		Qy	841 TTTATTACCAAAAGAAATAGAGTGAAPATCTGACGGGAAGAGTGCATGGGCAA 900
		Db	6816 TTTATTACCAAAAGAAATAGAGTGAAPATCTGACGGGAAGAGTGCATGGGCAA 6875

Qy	1981	CCACAGTAAAGGGCGCATGAACTTGTGTCAATTGTACTTTGCCCAATT	2040
Db	7956	CCACAGTAAAGGGCGCATGAACTTGTGTCAATTGTACTTTGCCCAATT	8015
Qy	2041	CATATGGATGATCAAGCAGTCACTGGATGAACTTGTGGAAAAGTGAG	2100
Db	8016	CATATGGATGATCAAGCAGTCACTGGATGAACTTGTGGAAAAGTGAG	8075
Qy	2101	CAACCTAGGCTTAGAATCTCAATCTATAGAACGCTACTAGCAAACCTTCAGTGGATGAACTTGTGGAAAAGTGAG	2160
Db	8076	CAACCTAGGCTTAGAATCTCAATCTATAGAACGCTACTAGCAAACCTTCAGTGGATGAACTTGTGGAAAAGTGAG	8135
Qy	2161	TGATATCTGACCGAGATAATTATCTTAATAGAACGCTACTCTGGAGAA	2220
Db	8136	TGATATCTGACCGAGATAATTATCTTAATAGAACGCTACTCTGGAGAA	8195
Qy	2221	CATATTCATTTATTGCTGAACTGAAACAGTAACTCTGTAAATAGACGTAACTT	2280
Db	8196	CATATTCATTTATTGCTGAACTGAAACAGTAACTCTGTAAATAGACGTAACTT	8255
Qy	2281	ATTATCPAAGGAGTAAGCAAACCTGATCTGAAGGATACCATCTGGAGGTATCT	2340
Db	8256	ATTATCPAAGGAGTAAGCAAACCTGATCTGAAGGATACCATCTGGAGGTATCT	8315
Qy	2341	GCTGTAACTATGCTGAACTGAAACAGTAACTCTGTAAATAGACGTAACTT	2400
Db	8316	GCTGTAACTATGCTGAACTGAAACAGTAACTCTGTAAATAGACGTAACTT	8375
Qy	2401	CAGAAAGCACACAGAAACATAAGAACACATGAAATTCCTCCAAACACTGTCAACC	2460
Db	8376	CAGAAAGCACACAGAAACATAAGAACACATGAAATTCCTCCAAACACTGTCAACC	8435
Qy	2461	AGAGCCTTCACACTCTGCTGAGGACAGTCTAACATCCATCATTAATGTGTCTACCA	2520
Db	8436	AGAGCCTTCACACTCTGCTGAGGACAGTCTAACATCCATCATTAATGTGTCTACCA	8495
Qy	2521	CATCTGGCTTACCGTSCTTACCAAGATTCTAGGACATGAACTGAAATGTTGCA	2580
Db	8496	CATCTGGCTTACCGTSCTTACCAAGATTCTAGGACATGAACTGAAATGTTGCA	8555
Qy	2581	GTGCCCTAATGCGAACCCCCAGATAAAGGAGGTGCTAGAAATTCCGAGGACATGGTGG	2640
Db	8556	GTGCCCTAATGCGAACCCCCAGATAAAGGAGGTGCTAGAAATTCCGAGGACATGGTGG	8615
Qy	2641	GGATCAGAACCTCTGGCTTGTGTTGAGTGCAGAGGGCCATAACTCTCTGGTTCGGAAAGGG	2700
Db	8616	GGATCAGAACCTCTGGCTTGTGTTGAGTGCAGAGGGCCATACTCTCTGGTTCGGAAAGGG	8675
Qy	2701	AAGAGGGTGGAGGTGAACTGTCCTGGAGGGAGGAATCTGCTTAAATCC	2760
Db	8676	AAGAGGGTGGAGGTGAACTGTCCTGGAGGGAGGAATCTGCTTAAATCC	8735
Qy	2761	CCAAAGGGAGGAACTGTAAAGTCCCGCTCCGAGGAACTGACGGGGAATGGCTGAG	2820
Db	8736	CCAAAGGGAGGAACTGTAAAGTCCCGCTCCGAGGAACTGACGGGGAATGGCTGAG	8795
Qy	2821	AGGTCTTAAGAAATCCGATTCCTGGAAAGGAGGGCTAAATTGTGGGGTTGACTTGC	2880
Db	8796	AGGTCTTAAGAAATCCGATTCCTGGAAAGGAGGGCTAAATTGTGGGGTTGACTTGC	8855
Qy	2881	AGGGGTTGGTGTGACTCTTGTGACTCTTGTGGTCCCTGGAAAGGAACTT	2940
Db	8856	AGGGGTTGGTGTGACTCTTGTGACTCTTGTGGTCCCTGGAAAGGAACTT	8915
Qy	2941	GGCTCCAGGGCTGGTGAAGGTAATGGGATCTCCTGATCTCAAGGGTCAGGGACT	3000
Db	8916	GGCTCCAGGGCTGGTGAAGGTAATGGGATCTCCTGATCTCAAGGGTCAGGGACT	8975
Qy	3001	GAGAGTGGCCATGCTTGTGACTCTTGTGGTCCCTGGAAAGGAACTT	3060
Db	8976	GAGAGTGGCCATGCTTGTGACTCTTGTGGTCCCTGGAAAGGAACTT	9035
Qy	3061	TACTCTCTAGTGTCAAGAGTGTGCTGCTGCAATGTGACATAATCTGACATA	3120

Disclosure; Fig 6A-H; 79pp; English.
The present sequence comprises a transcriptional regulatory element (TRE) from a human Glandular Kallikrein gene. The TRE is used to produce an adenoviral vector of the invention. The specification describes an adenovirus vector which comprises an adenovirus gene under transcriptional control of a cell status specific TRE. The TRE is preferably one that is essential for adenoviral propagation. The adenovirus vectors may be used for the treatment of a range of tumours such as lung, stomach, breast, colon and rectum, and uterine and cervix cancers.

Cy	1921	CCAGTTTGTGCTGGTAGAACTCATGAGAAGCTCCCTGGGTCAGAGGCCAAAAGATTTTATAC	1980	Qy	3001	GAGAGTTGCCATGCCATTGATCTTCCATCTACTCCTTAATCCACTTGTAGGGTAATCACC	3 060
Db	7896	CCAGTTTGTGCTGGTAGAACTCATGAGAAGCTCCCTGGGTCAGAGGCCAAAAGATTTTATAC	7955	Db	8976	GAGAGTTGCCATGCCATTGATCTTCCATCTACTCCTTAATCCACTTGTAGGGTAATCACC	9035
Qy	1981	CCACAGCTTAAGGAGGCGCATGAACTTCTGGTCACTTGTGCACTTGTGCCCCCAATT	2040	Qy	3061	TACTCTTCTAGTCACAAGAGTGGGCTGGAGATAATCTGCACATGTGCATGTC	3 120
Db	7956	CCACAGCTTAAGGAGGCGCATGAACTTCTGGTCACTTGTGCCCCCAATT	8015	Db	9036	TACTCTTCTAGTCACAAGAGTGGGCTGGAGATAATCTGCACATGTGCATGTC	9095
Qy	2041	CATATCGCATGATCNCGCACTTCAAGCTGATGACACAGGGTTTGCGGAAAGGTAG	2100	Qy	3121	CGAGGGCTGGGCACTCATCACTCATCACTCATCACTCATCACTCATCACTCATCACT	3 180
Db	8016	CATATGGATGATCATGAGCAGTTCAGGTGATGATGACACAGGGTTTGCGGAAAGGTAG	8075	Db	9096	CGAGGGCTGGGCACTCATCACTCATCACTCATCACTCATCACTCATCACTCATCACT	9155
Qy	2101	CAACCTAGGTTAGAAATCTCAATCTATAAGAGGACTACTAGAAACCTPTGTCAGTT	2160	Qy	3181	CCCATGACGTCATGAGCTGGAGCTGGAGCTTCCTCGTCACTGTCCTCAA	3 240
Db	8076	CAACCTAGGTTAGAAATCTCAATCTATAAGAGGACTACTAGAAACCTPTGTCAGTT	8135	Db	9156	CCCATGACGTCATGAGCTGGAGCTGGAGCTTCCTCGTCACTGTCCTCAA	9215
Qy	2161	TGTATCTGACCGAGATAATCTTATAATTGGGTTGAAGAGCACCTACTCTGGAGAA	2220	Qy	3241	CCATGGAGCTGTGAGCTGGGCTGGGATCTGGCTGGCTGGAGGGGG	3 300
Db	8136	TGTATCTGACCGAGATAATCTTATAATTGGGTTGAAGAGCACCTACTCTGGAGAA	8195	Db	9216	CCATGGAGCTGTGAGCTGGCTGGCTGGATCTGGCTGGCTGGAGGGGG	9275
Qy	2221	CATATTGTTATAATGTTCTGAACTGAAACATAACTCTGTTGAAAAATGAGCTTAACCTT	2280	Qy	3301	CCGGTSTCCGATTAAGATCTGAAACACAGGAACCGACTAAAGTGTAGAGAA	3 360
Db	8196	CATATTGTTATACTGTCCTGAACTGAAACATAACTCTGTTGAAAAATGAGCTTAACCTT	8255	Db	9276	CCTGGTCCGATTAAGATCTGAAACACAGGAACCGACTAAAGTGTAGAGAA	9335
Qy	2281	ATTATCTAAGGCACAACTGAACTGAACTGAGGGCATACATCTGCAGGCTATCT	2340	Qy	3361	TGGCATATGTGCTGTCATGATGAACTCTCAAGGACTCTGGTGGAGGGACAGGAGCT	3 420
Db	8256	ATTATCTAAGGCACAACTGAACTGAACTGAGGGCATACATCTGCAGGCTATCT	8315	Db	9336	TCACCATATGTGCTGTCATGAACTCTCAAGGACTCTGGTGGAGGGACAGGAGCT	9395
Qy	2341	GCTGTACAAATATGTTGAAAGATGGTCAGAAAGAAACCTGATATTGCTTGTCT	2400	Qy	3421	GAACHTACGGGTTGCCAGTCCACTGTCTCCAAAGTCAGTCTCCAGATACAGGCA	3 480
Db	8316	GCTGTACAAATATGTTGAAAGATGGTCAGAAAGAAACCTGATATTGCTTGTCT	8375	Db	9396	GAACHTACGGGTTGCCAGTCCACTGTCTCCAAAGTCAGTCTCCAGATACAGGCA	9455
Qy	2401	CAGANGACACAGAAACATAAGAGAACCATGGAAAATGTGTCACCAACTGTTAACCC	2460	Qy	3481	CTGTGCAAGCATCACTGACCTGATCTGACCATCTGACCATCTGACCATCTGAC	3 540
Db	8376	CAGAGACACAGAAACATAAGAGAACCATGGAAAATGTGTCACCAACTGTTAACCC	8435	Db	9456	CTGTGCAAGCATCACTGACCTGACCATCTGACCATCTGACCATCTGACCATCTGAC	9515
Qy	2461	AGAGCCTTCACACTTGTCTGAGGACAGCTCTAACATCCCATTTAGTGTCTACCA	2520	Qy	3541	ATGAACRCCATGGTGTCTGAGGAAACAGGGGTGAAGGCAATGGCTCTGTGTCTCAGA	3 600
Db	8436	AGAGCCTTCACACTTGTCTGAGGACAGCTCTAACATCCCATTTAGTGTCTACCA	8495	Db	9516	ATGAACRCCATGGTGTCTGAGGAAACAGGGGTGAAGGCAATGGCTCTGTGTCTCAGA	9575
Qy	2521	CATCTGGCTTACCGCTGCTAACAAAGATTCTAGGTCAAGTCATCCATTTGCA	2580	Qy	3601	GCCCCAGGGGCCATGACGGTGGGAGGGCTGGCTGGACTCTG	3 645
Db	8496	CATCTGGCTTACCGCTGCTAACAAAGATTCTAGGTCAAGTCATCCATTTGCA	8555	Db	9576	GCCAGAGGGCCATGACGGTGGGAGGGCTGGACTCTG	9620
Qy	2581	GTGCCCACTGCCAACCCGAAAGTAAGGGAGCTCAAGAAATCGAGGCAATGGTGG	2640	RESULT 4			
Db	8556	GTGCCCACTGCCAACCCGAAAGTAAGGGAGCTCAAGAAATCGAGGCAATGGTGG	8615	ID	AAA46552	standard; DNA; 12047 BP.	
Qy	2641	GGATGAGAATCTCTGGCTTGAGTCAGGGAGGGCCCATACACTCTGGTTCGGAAGGG	2700	XX	AAA46552;		
Db	8616	GGATGAGAATCTCTGGCTTGAGTCAGGGAGGGCCCATACACTCTGGTTCGGAAGGG	8675	AC			
Qy	2701	AAGGGCTGGAGGTGAATGTCCTGGCTGAGTCAGGGAGGGCCCATACACTCTGGTT	2760	DT	03-OCT-2000 (first entry)		
Db	8676	AAGGGCTGGAGGTGAATGTCCTGGCTGAGTCAGGGAGGGCCCATACACTCTGGTT	8735	XX			
Qy	2761	CCAAGGGAGAGCTGTAAGGTCAAGTCCAGTGGGACTGACTGAGTCAGGAAATGGCTGAG	2820	XX			
Db	8736	CCAAGGGAGAGCTGTAAGGTCAAGTCCAGTGGGACTGACTGAGTCAGGAAATGGCTGAG	8795	XX			
Qy	2821	AGGTCTAAGATCCGTATCTCTGGAGGGCTGAATGGGACTGAGTCAGGAAATGGCTGAG	2880	XX			
Db	8796	AGGTCTAAGATCCGTATCTCTGGAGGGCTGAATGGGACTGAGTCAGGAAATGGCTGAG	8855	XX			
Qy	2881	AGGGGTTGTTAGCTGGAGCTCTGGCTGGCTGGAGAAAGCAAGGACTGAACTT	2940	XX			
Db	8856	AGGGGTTGTTAGCTGGCTGGCTGGCTGGAGCTCTGGCTGGAGAAAGCAAGGACTGAACTT	8915	PR			
Qy	2941	GGCTCCAGGTTCGTTGGAGGTAAAGTCAAGGTCAGAGGACT	3000	PR			
Db	8916	GGCTCCAGGTTCGTTGGAGGTAAAGTCAAGGTCAGAGGACT	8975	XX			
				PI	Henderson DR, Yu D,		

Db	6576	CTACCATATAATGGTAATCTGGCTTGTGGAGTTCTGCAATTACATCCATTAACATCCGTATTA	6635
Qy	661	CATTCTTTACTTTAAAGTGGAAATAAGTGGCTCCCTCGAGAGTCAGGGTCTCAGAA	720
Pt	6636	CATTCTTTACTTTAAAGTGGAAATAAGTGGCTCCCTCGAGAGTCAGGGTCTCAGAA	6695
Pt	721	TGGCCCTTAACITCTGCATCAATTGAGTTCAAGGAGTCAGGGTCTCAGAA	780
Pt	6696	TGGCCCTTAACITCTGCATCAATTGAGTTCAAGGAGTCAGGGTCTCAGAA	6755
PS	6696	TGGCCCTTAACITCTGCATCAATTGAGTTCAAGGAGTCAGGGTCTCAGAA	6755
Qy	781	TCACTAATGTTGGPAGCCCTCATATAACTCAAAAGCTGTATGCTCATGGCTATGG	840
Db	6756	TCACTAATGTTGGPAGCCCTCATATAACTCAAAAGCTGTATGCTCATGGCTATGG	6815
Qy	841	TTTATTACAGAAAAGAATAGATGAATCTAACAGGAAGAGTTGATGGGGAAA	900
Db	6816	TTTATTACAGCAAAGAAATAGATGAATCTAACAGGAAGAGTTGATGGGGAAA	6875
Qy	901	GACAAGGAGACCTCCAAAGTAGGAAATCTAACAGGAAGAGTTGATGGGGAAA	960
Db	6876	GACAAGGAGACCTCCAAAGTAGGAAATCTAACAGGAAGAGTTGATGGGGAAA	6935
Qy	961	GCAGTATCTCTCCATACATGATGTTGTGATAATATTCAGTGTATGCCATACGGGAAC	1020
Db	6936	GCAGTATCTCTCCATACATGATGTTGTGATAATATTCAGTGTATGCCATACGGGAAC	6995
Qy	1021	TOAECTAGGCCTTGATATATTGGGACTCTGGTGCACAGACATGCGACCCCTCATGG	1080
Db	6996	TOAECTAGGCCTTGATATATTGGGACTCTGGTGCACAGACATGCGACCCCTCATGG	7055
Qy	1081	CTGAACTTGTACTGTTGCTTCAAGCGCTCTAAGCTGATAGCTGTAAACCAACATT	1140
Db	7056	CTGAACTTGTACTGTTGCTTCAAGCGCTCTAAGCTGATAGCTGTAAACACAG	7115
Qy	1141	GTCACCCATAATTCACATTGTTAGACTTACCTGGCTTCAAGCGCTCTAAGCTGATAGCTGTAAACACAG	1200
Db	7116	GTCACCCATAATTCACATTGTTAGACTTACCTGGCTTCAAGCGCTCTAAGCTGATAGCTGTAAACACAG	7175
Qy	1201	GCACTTAACAGGGGGAGGATATTCAAAAGCTTCAAGATGACCTCCAGSAGCTGATGCG	1260
Db	7176	GCACTTAACAGGGGGAGGATATTCAAAAGCTTCAAGATGACCTCCAGSAGCTGATGCG	7235
Qy	1261	AAGACGCTGGCTCTGGGAAAGGAAACCTTACCCGACACTTCCTTCAGGGCTT	1320
Db	7236	AAGACGCTGGCTCTGGGAAAGGAAACCTTACCCGACACTTCCTTCAGGGCTT	7295
Qy	1321	ATTTGGAGGATCAATGGGTCTATGGTGTGAGAACCCAGCACATGTCGGTGAGA	1380
Db	7296	ATTTGGAGGATCAATGGGTCTATGGTGTGAGAACCCAGCACATGTCGGTGAGA	7355
Qy	1381	GTGACTCTATGTGCTCAACATTGGCTTCAAGTGGCTAAGAAAGTATTAGCACTGGCTTCAG	1440
Db	7356	GTGACTCTATGTGCTCAACATTGGCTTCAAGTGGCTTCAAGAAAGTATTAGCACTGGCTTCAG	7415
Qy	1441	CACTCACAGAGCTCATCTTACATGGCTTCAAGGAGCTACTAGCCCTC	1500
Db	7416	CACTCACAGAGCTCATCTTACATGGCTTCAAGGAGCTACTAGCCCTC	7475
Qy	1501	ATTTGACAGAGAAAGACTGTGGATAAGAGGGGGTCAACAAATGTCAGACTCT	1560
Db	7476	ATTTGACAGAGAAAGACTGTGGATAAGAGGGGGTCAACAAATGTCAGACTCT	7535
Qy	1561	GTATGCTCTGGGGATCCTCTATGATACCGAGCCCCATATACTCTGCTGG	1620
Db	7536	GTATGCTCTGGGGATCCTCTATGATACCGAGCCCCATATACTCTGCTGG	7595
Qy	1681	TTGAGGTTATCTCAGACTCTCTATGATACCGAGCCCCATATACTCTGCTGG	1740
Db	7596	TTGAGGTTATCTCAGACTCTCTATGATACCGAGCCCCATATACTCTGCTGG	7715
Qy	1681	TTGAGGTTATCTCAGACTCTCTATGATACCGAGCCCCATATACTCTGCTGG	7715
Db	601	CTACCTATATAATGGTAATCTGGCTTGTGGAGTTCTACTGCAATTAA	660
Qy	541	TCCPTCTACCGTTATTCTCACCTAACCTTACCTGGCTCATTT	6455
Db	6396	TCCPTCTACCGTTATTCTCACCTAACCTTACCTGGCTCATTT	600
Qy	481	ACCTGGGTTCTGTTATAGGGTCAATGAACTTCAAGCTGATCAACTTTACAT	540
Db	6336	ACCTGGGTTCTGTTATAGGGTCAATGAACTTCAAGCTGATCAACTTTACAT	6395
Qy	421	CAACAAAACACCGAAATAACCAATTAGAACCTTCCCAACTCCCTGCAATTT	480
Db	6456	CAACAAAACACCGAAATAACCAATTAGAACCTTCCCAACTCCCTGCAATTT	6515
Qy	541	TCCPTCTACCGTTATTCTCACCTAACCTTACCTGGCTCATTT	6455
Db	6516	TCCPTCTACCGTTATTCTCACCTAACCTTACCTGGCTCATTT	6575

QY	1741	TCTCCCTTCCAGTCAGTCTTACTGCCATCTTCCAGGCCATCTCCAGCTGCAAGGTG	1800	Qy	2821	AGGTCTAAGAATCCCGTATCCTGGAAAGGGGGCTGAATTGTGAGGGTTGAGTTG	2880
Db	7716	TCTCCCTTCCAGTCAGTCTTACTGCCATCTTCCAGGCCATCTCCAGCTGCAAGGTG	7775	Db	8796	AGGTCTAAGAATCCCGTATCCTGGAAAGGGGGCTGAATTGTGAGGGTTGAGTTG	8855
QY	1801	TAGCCACAGTACCTTAACCTTGGAGAGAACATAAAGTGTATCCCTACGGGAGAAA	1860	Qy	2881	AGGGTTGGTTAGCTTGAGACTCTGGTCAAGGTGAGCTTCCTGGGGTCTGGAAAGGAA	2940
Db	7776	TAGCCACAGTACCTTAACCTTGGAGAGAACATAAAGTGTATCCCTACGGGAGAAA	7835	Db	8856	AGGGTTGGTTAGCTTGAGACTCTGGTCAAGGTGAGCTTCCTGGGGTCTGGAAAGGAA	8915
QY	1861	AAAAAAAGAAACTCTGAAAGAGCTGACATTACCGACTTACGGACAAACACA	1920	Qy	2941	GGCTCCAGGGTTGGTGTGAGGTAATGGGATCTCTGATTCTCAAGGGTCAGGGACT	3000
Db	7836	AAAAAAAGAAACTCTGAAAGAGCTGACATTACCGACTTACGGACAAACACA	7895	Db	8916	GGCTCCAGGGTTGGTGTGAGGTAATGGGATCTCTGATTCTCAAGGGTCAGGGACT	8975
QY	1921	CCAGGTTTGTGCTGGTAGAACTCATGAGACTCTCTGGTGAGCCAAAGATTTAAC	1980	Qy	3001	GAGAGTTGCCATTGCTTGTGATCTGGTCAAGGTGAGCTTACTCCACCTTGAAGGTAA	3060
Db	7896	CCAGGTTTGTGCTGGTAGAACTCATGAGACTCTCTGGTGAGCCAAAGATTTAAC	7955	Db	8976	GAGAGTTGCCATTGCTTGTGATCTGGTCAAGGTGAGCTTACTCCACCTTGAAGGTAA	9015
QY	1981	CCACAGCTAGGAGCGAGTGAACCTTGTGTCAGTTGTCATCTGGCCCCAATT	2040	Qy	3061	TACTCTCTAGTTCCACAAAGTGGGCCCTCGCAGGTTAATCTCCACATGTGCCATGTC	3120
Db	7956	CCACAGCTAGGAGCGAGTGAACCTTGTGTCAGTTGTCATCTGGCCCCAATT	8015	Db	9036	TACTCTCTAGTTCCACAAAGTGGGCCCTCGCAGGTTAATCTCCACATGTGCCATGTC	9095
QY	2041	CATATGGATGATCAGGAGGTTCAAGGTGATGACAAAGGGTTGGCAAAAGGTGAG	2100	Qy	3121	CGGAGGCTGGGGATCATCCACCTATCCACATCTGGATCTGGCTATGCGGCGCG	3180
Db	8016	CATATGGATGATCAGGAGGTTCAAGGTGATGACAAAGGGTTGGCAAAAGGTGAG	8075	Db	9096	CGGAGGCTGGGGATCATCCACCTATCCACATCTGGATCTGGCTATGCGGCGCG	9155
QY	2101	CAACCTAGGTTAGAAATCCCAATCTTATAAGGAACTTACCAAACCTTGTCCAGTCT	2160	Qy	3181	CGCCATGAGTCATAGCTGAGCTAGCTGAGCTTCTAGAAACCAGGACTGAAAGSTGCTAAGAGAA	3240
Db	8076	CAACCTAGGTTAGAAATCCCAATCTTATAAGGAACTTACCAAACCTTGTCCAGTCT	8135	Db	9156	CGCCATGAGTCATAGCTGAGCTAGCTGAGCTTCTCTGZGCGCCCTCTCCGTCAGTCCCAGA	9215
QY	2161	TGTATCTGACGGAGATAATTATGCTTATAATTGCTTGAAGAGACCTACTCTGGAGAA	2220	Qy	3241	CCATGGAGCTGTGGAGCTGGCTCCCTGGTGGATCTGGCTGGCTGGCAGCCGGGG	3300
Db	8136	TGTATCTGACGGAGATAATTATGCTTATAATTGCTTGAAGAGACCTACTCTGGAGAA	8195	Db	9216	CCATGGAGCTGTGGAGCTGGCTCCCTGGTGGATCTGGCTGGCAGCCGGGG	9275
QY	2221	CATATTGATTATTGTCCTGAACAGTAAACAATTCTGTAAATAAGTACGTTAACATT	2280	Qy	3301	CCTGGTGTGGATAAGATCTAGAAACCAGGACTGAAAGSTGCTAAGAGAA	3360
Db	8196	CATATTGATTATTGTCCTGAACAGTAAACAATTCTGTAAATAAGTACGTTAACATT	8255	Db	9276	CCTGGTGTCCGATAAGATCTAGAAACCAGGACTAAGTGTGAGAA	9335
QY	2281	ATTATCTAAGGCACTAGGAACCTAGTCTGAGGGCATAACATCTGCAAGGCTATCT	2340	Qy	3361	TGGCCATATGCGCTCCATGAAATTCTCAAGGACTTCTGGGTGAGGGCACAGGCTT	3420
Db	8256	ATTATCTAAGGCACTAGGAACCTAGTCTGAGGGCATAACATCTGCAAGGCTATCT	8315	Db	9336	TGGCCATATGCGCTCCATGAAATTCTCAAGGACTTCTGGGTGAGGGCACAGGCTT	9395
QY	2341	GCTGTACAAATACTCTTGAAGAAGTGTCCAGAAAAGGAAACGTTATTGCTTGTCT	2400	Qy	3421	GAACATCAGGCTTGTGCCAGTCTCCTGTCAGTCTCCCGATAACAGGCA	3480
Db	8316	GCTGTACAAATACTCTTGAAGAAGTGTCCAGAAAAGGAAACGTTATTGCTTGTCT	8375	Db	9396	GAACATCAGGCTTGTGCCAGTCTCCTGTCAGTCTCCCGATAACAGGCA	9455
QY	2401	CAGAGACACACAGAAATAAGAGAACTTGTCTCCAAACACTCTGTTAACCC	2460	Qy	3481	CTGTGCAGCATGAGTTCAATCTGTACCAATCTGTGAACTCCAGGACCTCTG	3540
Db	8376	CAGAGACACACAGAAATAAGAGAACTTGTCTCCAAACACTCTGTTAACCC	8435	Db	9456	CTGTGCAGCATGAGTTCAATCTGTACCAATCTGTGAACTCCAGGACCTCTG	9515
QY	2461	AGAGCCTCCACTCTGTCTGAGGACAGTCTTAACTCCCATCTTGTGTCATCA	2520	Qy	3541	ATGAACCATGTTGTGAGGGAGGGCTGAGGCTGAGCTCCCTGTCATCTCAGA	3600
Db	8436	AGAGCCTCCACTCTGTCTGAGGACAGTCTTAACTCCCATCTTGTGTCATCA	8495	Db	9516	ATGAACCATGTTGTGAGGGAGGGCTGAGCTCCCTGTCATCTCAGA	9575
QY	2521	CATCTGGCTTCACTGGCTTAACCAAGATTCTAGGTCAGTCTCCACCTGTCATCC	2580	Qy	3601	GCCCAAGGGGCCATGACGGTGGGAGGGCTGTGAACTGGC	3645
Db	8496	CATCTGGCTTCACTGGCTTAACCAAGATTCTAGGTCAGTCTCCACCTGTCATCC	8555	Db	9576	GCCCAAGGGGCCATGACGGTGGGAGGGCTGTGAACTGGC	9620
QY	2581	GTGCCCACTGCCAACCCCGATAACAGGTTCTGGTCAAGGAGATGGGG	2640	RESULT 5			
Db	8556	GTGCCCACTGCCAACCCCGATAACAGGTTCTGGTCAAGGAGATGGGG	8615	AAH43617			
QY	2641	GGATCAGAACCTCTGGCTGAGTGTGAGGGGGCTTCTGGTCAAGGAGATGGGG	2700	ID	AAH43617	standard; cDNA;	12047 BP.
Db	8616	GGATCAGAACCTCTGGCTGAGTGTGAGGGGGCTTCTGGTCAAGGAGATGGGG	8675	XX	AAH43617;		
QY	2701	AAGAGGTCAGGTCAGTCTGGTCAAGGAGATGGGGCTTCTGGTCAAGGAGATGGGG	2760	XX	AAH43617;		
Db	8676	AAGAGGTCAGGTCAGTCTGGTCAAGGAGATGGGGCTTCTGGTCAAGGAGATGGGG	8735	DT	07-JAN-2002	(first entry)	
QY	2761	CCAAGGGAGAGATGCTTAAGGTCAGGCTTCCAGTGTGAGGCTCTGAG	2820	XX	Human glandular kallikrein-TRE.		
Db	8736	CCAAGGGAGAGATGCTTAAGGTCAGGCTTCCAGTGTGAGGCTCTGAG	8795	KW	Adenovirus; AdP; replication-competent; adenoviral vector; TRE; PCR;		
			KW	transcriptional regulatory element; mutation; deletion; IRES; Primer;			
			KW	promoter; internal ribosome entry site; cytotoxic; cancer; bladder;			
			KW	amplify; Polymerase chain reaction; alpha-Fetoprotein; AFP; Emcv;			
			KW	encephalomyarditis virus; vascular endothelial growth factor; VEGF;			
			KW	immunoglobulin heavy-chain binding protein; Bip; uropakin II; PDGF;			

Db	7356	GTA GCT TCA TAT GTG GTG CTA AAC ATG CTG TGA GAG AAG AT TAA CGC AT GG CT TCA G	7415	Qy	2521	CAT CTG GCT TCA ACC AAG AT TCA CCT GAG TCC AGT TCC CAG AT TCC CAC CA TGG GCA	2580
Qy	1441	CACTCAAGATGCTCATCPAATCTCATGCTAACATGGCTAACAGGTGGACTACTAGCTC	1500	Db	8496	CAT CTG GCT TCA ACC AAG AT TCA CCT GAG AT TCC CAC CA TGG GCA	8555
Db	7416	CACTCAAGATGCTCATCPAATCTCATGCTAACATGGCTAACAGGTGGACTACTAGCTC	7475	Qy	2581	GTGCCCACTGCGAACCCACAAATPACGGAGTCAGATTCCAGGGACATGGCTG	2640
Qy	1501	ATTGACAGGAAAGGACTTGTTGATAAGAAGGGGTTGACCAATAGGTCAGATCTT	1560	Db	8556	GTGCCCACTGCGAACCCACAAATPACGGAGTCAGATTCCAGGGACATGGCTG	8615
Db	7476	ATTGACAGGAAAGGACTTGTTGATAAGAAGGGGTTGACCAATAGGTCAGATCTT	7535	Qy	2641	GGATCAGAACCTCTGGCTTGAGTGAAGGGGGCAATACTCTGGTCCGANGGAGG	2700
Qy	1561	GGATGCAAGGGCTCAGGACCATGTTAGACATGGCTGAGAATAATGGCTG	1620	Db	8616	GGATCAGAACCTCTGGCTTGAGTGAAGGGGGCAATACTCTGGTCCGANGGAGG	8675
Db	7536	GGATGCAAGGGCTCAGGACCATGTTAGACATGGCTGAGAATAATGGCTG	7595	Qy	2701	AAGGGTGGAGGTTGATGCTTGAGGAGGATGTTGAACTCTTAATCC	2760
Qy	1621	ATGTCCTGCCCCGAAAGGGGATGCACTTCCTGACCCCTATCTCAGATCTTGACT	1680	Db	8676	AAGGGCTGGAGGTTGATGCTTGAGGAGGATGTTGAACTCTTAATCC	8735
Db	7596	ATGTCCTGCCCCGAAAGGGGATGCACTTCCTGACCCCTATCTCAGATCTTGACT	7655	Qy	2761	CCAGGGAGGAGACTGTTAAGGTCCAGCTCAGGAGACTGTCGGGAAATGGCTGAG	2820
Qy	1681	TGAGGTAACTCTCAGACTCTCTCATGATAACCAGGGCCATATACTCTGTG	1740	Db	8736	CCAGGGAGGAGACTGTTAAGGTCCAGCTCAGTTCGGGTTACTGACCTGGGATGGCTGAG	8795
Db	7656	TGAGGTAACTCTCAGACTCTCTCATGATAACCAGGGCCATATACTCTGTG	7715	Qy	2821	AGGTCTAAGAATCCGTAATCTCGGAAAGGAGGCTGAAATTGTTGAGGGTTGAGTTGC	2880
Qy	1741	TCTCCCTTCTCAGCTTACTGCCACTCTCCAGCTCCATCTCCAGCTGGCCAGTG	1800	Db	8796	AGGTCTAAGAATCCGTAATCTCGGAAAGGAGGCTGAAATTGTTGAGGGTTGAGTTGC	8855
Db	7716	TCTCCCTTCTCAGCTTACTGCCACTCTCCAGCTCCATCTCCAGCTGGCCAGTG	7775	Qy	2881	AGGGTTGTTAGCTTGAGACTCCCTGGTGGATGGAAAGCAGGACTCTGGAACATT	2940
Qy	1801	TAGCCACATGACCTAACCTCTTGAAGAGAACTATAATGTTGATCCTCAAGGAGAAA	1860	Db	8856	ACGGTTGTTAGCTGAGCTCTGGCTGAGACTCTGGCTGAGACTCTGGAACATT	8915
Db	7776	TAGCCACATGACCTAACCTCTTGAAGAGAACTATAATGTTGATCCTCAAGGAGAAA	7835	Qy	2941	GGCTCAGGGTTGGTGGATGGTGGATGGTGGATGGTGGATGGTGGACT	3000
Qy	1861	AAAAAAAGGAACTCTCAAAGGCTGACATTTACGGACTCTGCAACACTAAAGCTTACCTG	1920	Db	8916	GGCTCAGGGTTGGTGGATGGTGGATGGTGGATGGTGGACT	8975
Db	7836	AAAAAAAGGAACTCTCAAAGGCTGACATTTACGGACTCTGCAACACTAAAGCTTACCTG	7895	Qy	3001	GAGAGTGGCCATGCTTGTGACTCTTCACTCTTCACTCTTCACTCTTCACTCTTCA	3060
Qy	1921	CCAGCTTAAGGSCAGGACTCATGAGACTCTGGGTCAAGGCCAAAGATTATTAC	1980	Db	8976	GAGAGTGGCCATGCTTGTGACTCTTCACTCTTCACTCTTCACTCTTCACTCTTCA	9035
Db	7896	CCAGCTTAAGGSCAGGACTCATGAGACTCTGGGTCAAGGCCAAAGATTATTAC	7955	Qy	3061	TACTCTCTAGTCTAGTCCACAAGGCTCCCTGGGAGACTATACTGTCACATGTCATGTC	3120
Qy	1981	CCAGCTTAAGGSCAGGACTCATGAGACTCTGGGTCAAGGCCAAATT	2040	Db	9036	TACTCTCTAGTCTAGTCCACAAGGCTCCCTGGGCTCTGTCACATGTCATGTC	9095
Db	7956	CCAGCTTAAGGSCAGGACTCATGAGACTCTGGGTCAAGGCCAAATT	8015	Qy	3121	CCGAGGCTGGCCATGCTTGTGACTCTTCACTCTTCACTCTTCACTCTTCA	3180
Qy	2041	CATATGGCATCACAGGACTTGGCTGAGTCACTTCACTTATAAGGACTACGTTG	2100	Db	9096	CCGAGGCTGGCCATGCTTGTGACTCTTCACTCTTCACTCTTCACTCTTCA	9155
Db	8016	CATATGGCATCACAGGACTTGGCTGAGTCACTTCACTTATAAGGACTACGTTG	8075	Qy	3181	CGCCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTG	3244
Qy	2101	CAACCTGGTTGAGAACTCTCACTTATAAGGACTACCACTTGTCCAGTT	2160	Db	9156	CGCCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTG	9215
Db	8076	CAACCTGGTTGAGAACTCTCACTTATAAGGACTACCACTTGTCCAGTT	8135	Qy	3241	CCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTG	3300
Qy	2161	TGATCTGAGGAGATAATTCTTATAATTGGTTGAAAGCTACTCTGGAGAA	2220	Db	9216	CCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTGTCATGAGCTG	9275
Db	8136	TGATCTGAGGAGATAATTCTTATAATTGGTTGAAAGCTACTCTGGAGAA	8195	Qy	3301	CCTGGTCTCCGATAAAGATCTGAGACCAAGGAACCAAGGACTAAAGGTGTA	3360
Qy	2221	CATATTGATTATTGTCCTGAAAGTAAACATCTGTTGAAATAGACGTTAACCTT	2280	Db	9276	CCTGGTCTCCGATAAAGATCTGAGACCAAGGACTAAAGGTGTA	9335
Db	8196	CATATTGATTATTGTCCTGAAAGTAAACATCTGTTGAAATAGACGTTAACCTT	8255	Qy	3361	TGGCCATATGTCGCTGTCATGAAATCTCAAGGACTTCGGGTGAGGGACAGGAGCT	3420
Qy	2281	ATTATCTAAGGCACTTAAGGCAAACTACATCTGAGGCCATACCATCTGCAAGGCTTAC	2340	Db	9336	TGGCCATATGTCGCTGTCATGAAATCTCAAGGACTTCGGGTGAGGGACAGGAGCT	9395
Db	8256	ATTATCTAAGGCACTTAAGGCAAACTACATCTGAGGCCATACCATCTGCAAGGCTTAC	8315	Qy	3421	GAACCTAACGGTTGGCTCCACATCTGAGCTTCCAGATAACGGGCA	3480
Qy	2341	GCTGACAAATATGTTGAAAGATGGCCAGAAGAACCTGTTATTCGCTTGT	2400	Db	9396	GAACCTAACGGTTGGCTCCACATCTGAGCTTCCAGATAACGGGCA	9455
Db	8316	GCTGACAAATATGTTGAAAGATGGCTCCAGAAAAGGAAACCTGTTCTT	8375	Qy	3481	CTGGCCAGCATGAGCTTCACTCTGAGCTTCACTCTGAGCTTACGGGCCCTG	3540
Qy	2401	CAGAAGAACAGAACATAAGGAAACCATGGAAATCTCCATCAACTGTTAAC	2460	Db	9456	CTGGCCAGCATGAGCTTCACTCTGAGCTTCACTCTGAGCTTACGGGCCCTG	9515
Db	8376	CAGAAGAACAGAACATAAGGAAACCATGGAAATCTCCATCAACTGTTAAC	8435	Qy	3541	ATGAACACCTGTCAGTGTGAGGAAAGGGGGTGAAGCTCTCTGTGTGTCAGA	3600
Qy	2461	AGAGCCTCOACTCTGTCAGGACAGCTTACATCCATCAACTGTTAAC	2520	Db	9516	ATGAACACCTGTCAGTGTGAGGAAAGGGGGTGAAGCTCTCTGTGTGTCAGA	9575
Db	8436	AGAGCCTCOACTCTGTCAGGACAGCTTACATCCATCAACTGTTAAC	8495				

Db	7176	GCACTTAAACGGGAGGATATTCAAAGCTTAGAGATGACCCCTCCAGGCTGAAATGC	7235	Qy	2341	GCTGTACAAATAATGGCTGAAAGAAGCTCCAGAAAGAAACGGTATTATGGCTTGTCT	2400
Qy	1261	AAAGACCTGGCCTTTGGCAAGGAAATCCTTACCCSACACTCTCCTTCAGGGTT	1320	Db	8316	GTTGTAATAATGGCTGAAAGGTTCCGAAGAAACGTATTATGGCTTGTCT	8375
Db	7236	AAAGACCTGGCCTTTGGCAAGGAAATCCTTACCCSACACTCTCCTTCAGGGTT	7295	Qy	2401	CAGAAGBACACAGAACATATAAGGAAACCATTGAAACATCCCAACACTGTTACCC	2460
Qy	1321	ATTGGAGGTCAANTGGTCACTGTGTGACACCGCACATGTGTGZAGA	1380	Db	8376	CAGAAGACACAGAACATATAAGGAAACCATTGAAACATCCCAACACTGTTACCC	8435
Db	7296	ATTGGAGGTCAATGTGTCACTGTGTGACACCGCACATGTGTGZAGA	7355	Qy	2461	AGAGCCCTCCACTCTGTCTGAGACAGCTTAACTCCATCATTAGGTGTCATCCA	2520
Qy	1381	GTGACTTCTATGTGTGCTAACATGTGTGAGTGGTAAAGAAATTAGGATGSCCTTCA	1440	Db	8436	AGAGCCCTCCACTCTGTCTGAGACAGCTTAACTCCATCATTAGGTGTCATCCA	8495
Db	7356	GTGACTTCTATGTGTGCTAACATGTGTGAGTGGTAAAGAAATTAGGATGSCCTTCA	7415	Qy	2521	CATCTGCTTACCGTGCCPACACAGATTCTGAGTCCAGTTCAGTCCAGTTGGCA	2580
Qy	1441	CACTCACAGATGCTCATCTCATCTAACATGCTACGGGTCGCAACTAGGCTC	1500	Db	8496	CATCTGCTTACCGTGCCPACACAGATTCTGAGTCCAGTTCAGTCCAGTTGGCA	8555
Db	7416	CACTCACAGATGCTCATCTCATCTAACATGCTACGGGTCGCAACTAGGCTC	7475	Qy	2581	GTGCCCAACTGCAACCCGAAATAGGGACTGTAAGATTCCAGGGACATGGTGG	2640
Qy	1501	ATTGACAGAACAGAACATGCTAACATGCTACGGGTCGCAATTAGGCTCATCT	1560	Db	8556	GTGCCCAACTGCAACCCGAAATAGGGACTGTAAGATTCCAGGGACATGGTGG	8615
Db	7476	ATTGACAGAACAGAACATGCTAACATGCTACGGGTCGCAATTAGGCTCATCT	7535	Qy	2641	GTATCAGAAACTCTGGCTTCACTGTGAGTGGAGGGCCATACTCCCTGTTGGAGG	2700
Qy	1561	GGATGCAAGGGCTCAGGACCATGATTAGACATTGCTGAGAAAATTGGCTGG	1620	Db	8616	GTATCAGAAACTCTGGCTTCACTGTGAGTGGAGGGCCATACTCCCTGTTGGAGG	8675
Db	7536	GGATGCAAGGGCTCAGGACCATGATTAGACATTGCTGAGAAAATTGGCTGG	7595	Qy	2701	AGAGGCTGGAGGAGTGGATGGCTGGGGAGGAATGGCTGGTTGAACTCTTAATCC	2760
Qy	1621	ATGTCCTGCCCCGAAAGGGGATGCACTTCTGACCCSTATCTCAGATCTGACT	1680	Db	8676	AGAGGCTGGAGGAGTGGATGGCTGGTTGAACTGCTGGTGTGAACTCTTAATCC	8735
Db	7596	ATGTCCTGCCCCGAAAGGGGATGCACTTCTGACCCSTATCTCAGATCTGACT	7655	Qy	2761	CCAGGGAGGAGACTGTAAGGTCTGGCTTCACTGCTCCAGGTAATGGGCTGAG	2820
Qy	1681	TGAGGTATTCTGAGCTTCTGAGTACCAAGGCCCATAATACTCTGTGICC	1740	Db	8736	CCAGGGAGGAGACTGTAAGGTCTGGCTTCACTGCTCCAGGTAATGGGCTGAG	8795
Db	7656	TGAGGTATTCTGAGCTTCTGAGTACCAAGGCCCATAATACTCTGTGICC	7715	Qy	2821	AGTCTAGAAATCCGTATCTCGGAACTCTCCACCTGCACTGGTGAATTGTGAGG	2880
Qy	1741	TCTCCCTTCTCAGCTTACTGCCCACCTTCCAGCTTCTCAGCTTCTGAGGTG	1800	Db	8796	AGSTCTAAGAAUTCCGTATCTCGGAAAGGGGCTGTAATTGTGAGG	8855
Db	7716	TCTCCCTTCTCAGCTTACTGCCCACCTTCCAGCTTCTCAGCTTCTGAGGTG	7775	Qy	2881	AGGGTTGTTAGCTTAACTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAG	2940
Qy	1801	TAGCCACAGTACCTAACTCTTGCAGAGAACTATAATGGTATCCTACGGGAGAAA	1860	Db	8856	AGGGTTGTTAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAG	8915
Db	7776	TAGCCACAGTACCTAACTCTTGCAGAGAACTATAATGGTATCCTACGGGAGAAA	7835	Qy	2941	CCCTCAGGGTTGGTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAG	3000
Qy	1861	AAAAAGAACTCTAAAGACCTGACATTACCGACTTACAGCTTACAGCTTACCTG	1920	Db	8916	GCTCCAGGGTTGGTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAG	8975
Db	7836	AAAAAGAACTCTAAAGACCTGACATTACCGACTTACAGCTTACCTG	7895	Qy	3001	GAGATGTCGCCATGCTTGTCTTCCATCTACTCCATTCTGAGGTAACTCACC	3060
Qy	1921	CGAGTTTGCTGTGTAAGACTCATGAACTCTGGGTAGAGCAATTATTCAC	1980	Db	8976	GAGATGTCGCCATGCTTGTCTTCCATCTACTCCATTCTGAGCTTCTGAG	9035
Db	7896	CGAGTTTGCTGTGTAAGACTCATGAACTCTGGGTAGAGCAATTATTCAC	7955	Qy	3061	TACTCTCTAGTCTCAAGACTGCTGCTCTGGCACTTATGTCACATGCTGAT	3120
Qy	1981	COACAGCTAACGGGAGCATGAACTTGTGTGTTACATTGTTCACTGCCCATT	2040	Db	9036	TACTCTCTAGTCTCAAGACTGCTGCTCTGGCACTTATGTCACATGCTGAT	9095
Db	7956	CCACAGCTAACGGGAGCATGAACTTGTGTGTTACATTGTTCACTGCCCATT	8015	Qy	3121	CCAGGCTGGGCACTCATCACTCATCACTCATCACTCATCACTCATCACT	3180
Qy	2041	CATATGGATGATCAGACAGTTCAGGTGGATGGACACAGGGTTGTGCAAAGGTGAG	2100	Db	9096	CCAGGCTGGGCACTCATCACTCATCACTCATCACTCATCACTCATCACT	9155
Db	8016	CATATGGATCAGACAGTTCAGGTGGATGGACACAGGGTTGTGCAAAGGTGAG	8075	Qy	3181	CGCATGAGCTGTCAGTGTGAGCTGGGACTTCCCTGAGGCTCTCCGTAAGT	3240
Qy	2101	CAACCTTAAGCTTAACTCTCAAACTTAACTAGAACCTGTCAGTCTT	2160	Db	9156	CGCATGAGCTGTCAGTGTGAGCTGGGACTTCCCTGAGGCTCTCCGTAAGT	9215
Db	8076	CAACCTTAAGCTTAACTCTCAAACTTAACTAGAACCTGTCAGTCTT	8135	Qy	3241	CCATGGAGCTGGGACTCTGGCTGCTGCTGGCTGCTGGCTGCTGGCTGCTGG	3300
Qy	2161	TGATCTGACCGAGATTACTTAACTTATGGTTGAGCAGACCTACTCTGGAGAA	2220	Db	9216	CCATGGAGCTGGGACTCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG	9275
Db	8136	TGATCTGACCGAGATTACTTAACTTATGGTTGAGCAGACCTACTCTGGAGAA	8195	Qy	3301	CTCTGGTGTGCGATAAGATCTGAAACGAAACGAAACTCTGGCTGCTGGCTG	3360
Qy	2221	CATATGTTATTATGCTGCAAGTAAACAAATCTGCTGAAATAAACGTTAACTT	2280	Db	9276	CTCTGGTGTGCGATAAGATCTGAAACGAAACGAAACTCTGGCTGCTGGCTG	9335
Db	8196	CATATGTTATTATGCTGCAAGTAAACAAATCTGCTGAAATAAACGTTAACTT	8255	Qy	3361	TGGCCATPATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3420
Qy	2281	ATTATCAAGCTAACGGCTAACCTGAACTGCAAGGCTTCACTCTGGCTT	2340	Db	9336	TGGCCATPATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	9395
Db	8256	ATTATCAAGCTAACGGCTAACCTGAACTGCAAGGCTTCACTCTGGCTT	8315				

Db	9216	CCATGAGGTGGACTGCTGGTCCCCTGGCTGTCAGGGAGGGGG 9275	PS	Disclosure: Fig 16; 83bp; English.
Qy	3301	CCTGGTGTCCGATAAGATCCTAGAACCAAGACTGAAAGCTGCTAGAGAA 3360	XX	The present invention relates to adenoviral vectors comprising an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element (TRE). Example TREs given in the specification include human prostate-specific antigen (PSA) TRE, human glandular kallikrein (hKLK) TRE, rat probasin (PB) TRE, human carcinomaembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3 (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for introducing new genetic capability, particularly associated with cytotoxicity for treating neoplasia. For example, the vector may be used in a target cell to suppress tumour growth, or to kill the target cell. The vector is particularly useful in gene therapy. The present sequence represents a TRE.
Db	9276	CCTGGTGTCCGATAAGATCCTAGAACCAAGACTGAAAGCTGCTAGAGAA 9335	CC	
Db	3361	TGGCCATATCGCTGCCTGAATTCTAGGAACTTCTGGTGGAGGCT 3420	CC	
Qy	9336	TGGCCATATCGCTGCCTGAATTCTAGGAACTTCTGGTGGAGGCT 9395	CC	
Db	3421	GAACTTACGGGTTGCCCATGAGTCTCCAAAGATAAGGAA 3480	CC	
Db	9396	GAACTTACGGGTTGCCCATGAGTCTCCAAAGATAAGGAA 9455	CC	
Qy	3481	CTGTCGCCAGATCAGCTCTCTGTACCATCTGAAAGGACTACCAGGACCCCTG 3540	XX	
Db	9456	CTGTCGCCAGATCAGCTCTCTGTACCATCTGAAAGGACTACCAGGACCCCTG 9515	XX	
Qy	3541	ATGAAACACATGGGCTGTGGAGGAAAGGATGGACTCTGGTGTCAAA 3600	Qy	Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other; Score 100.0%; Pred. No. 0; Indels 0; Gaps 0;
Db	9516	ATGAAACACATGGGCTGTGGAGGAAAGGCTGGTGTCAAA 9575	Db	5976 GGCCTCAATAATGTTAAGGTGTAATGTCAGGAAATGTTGAAACTA 60
Qy	3601	GCCCCAGGGGCATGACGGTGGGGTGTGGGACTCTGGACTGGC 3615	Qy	1 GGCCCTCAATAATGTTAAGGTGTAATGTCAGGAAATGTTGAAACTA 60
Db	9576	GCCCCAGGGGCATGACGGTGGGGTGTGGGACTCTGGACTGGC 96210	Db	5976 GGCCTCAATAATGTTAAGGTGTAATGTCAGGAAATGTTGAAACTA 60
RESULT 8			Qy	61 CTGTCGCCAGATGTTCTGAGTCTAGGTGTTGGCTGGCTGGCTGGT 120
ACD07307	ID	ACD07307 standard; DNA: 12047 BP.	Db	6036 CTGTCGCCAGATGTTCTGAGTCTAGGTGTTGGCTGGCTGGT 6095
AC			Qy	121 CTTAGCCCTGAAATCAGGAGTATGGGTGAAGCTTGAGCTTGAGCTGG 180
XX			Db	6096 CTTAGCCCTGAAATCAGGAGTATGGGTGAAGCTTGAGCTGG 6155
DT			Qy	181 GTTGGCTTCGGGACACATTTGACATGTTGGACTGTGATTGTTGTC 240
XX			Db	6156 GTTGGCTTCGGGACACATTTGACATGTTGGACTGTGATTGTTGTC 6215
DE			Qy	241 TCTGAATCTTAATGTCCTGAGGCATCTAGAAATCTGAAATCTGAAATTCTG 300
XX			Db	6216 TCTGAATCTTAATGTCCTGAGGCATCTAGAAATCTGAAATTCTGAAATTCTG 6275
KW			Qy	301 ATTATCTTCAAGTAGGACATCTCCAGTCTGGCTGGAGCTGTGACT 360
KW			Db	6276 ATTATCTTCAAGTAGGACATCTCCAGTCTGGCTGGAGCTGTGACT 6335
KW			Qy	361 CAGTGACCCGGCTGGCAATTCACTCATATAAGTGGGCTATCTTGGCTCATGTT 420
KW			Db	6336 CAGTGACCCGGCTGGCAATTCACTCATATAAGTGGGCTATCTTGGCTCATGTT 6395
KW			Qy	421 CAACCAAACACCGAAATAACCATAGAACCTTCCCTGAGCTGCAATGTTAA 480
KW			Db	6396 CAACCAAACACCGAAATAACCATAGAACCTTCCCTGAGCTGCAATGTTAA 6455
KW			Qy	481 ACCTGGATTTCCTGTTAAATGGTTCATGATAAATTCTGAGCTGATC 540
KW			Db	6456 ACCTGGATTTCCTGTTAAATGGTTCATGATAAATTCTGAGCTGATC 6515
KW			Qy	541 TCCCTCTACGGTATTCTCACCCACCTTAAATGATCTCCCATATATCCCTGATT 600
KW			Db	6516 TCCCTCTACGGTATTCTCACCCACCTTAAATGATCTCCCATATATCCCTGATT 6575
KW			Qy	601 CTACCTTAAATGGTAAATCTGGTTTGCAGTTTACTGATACTCTGTTAA 660
KW			Db	6576 CTACCTTAAATGGTAACTCTGGTTTGCAGTTTACTGATACTCTGTTAA 6635
OS			Qy	661 CATTCTTACTTAAATGGAAATAAGTGGCTGGAGTTCAAGA 720
Homo sapiens.			Db	6635 CATTCTTACTTAAATGGAAATAAGTGGCTGGAGTTCAAGA 6695
XX			Qy	721 TGGCCCTTACTCTGACATCAATGGATTCAAGGAGTCATCTCAGGT 780
PN			Db	6696 TGGCCCTTACTCTGACATCAATGGATTCAAGGAGTCATCTCAGGT 6755
XX			Qy	(HEND/) HENDERSON D. R. (SCHU) SCHUUR E. R.
PD			Db	Hender son DR, Schuur ER; DR / 2003-456547/43.
XX			Qy	New adenovirus vector for transfecting target host cells, comprises an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element.

426	AAACACCGATAAACCTTAACTCCCACTTCCAGCTGAACTTAAACCTA	485	Dy
6401	AAACACCGATAAACCTTAACTCCCACTTCCAGCTGAACTTAAACCTA	6460	Db
486	GGATTCGTTAAAGGTGATCAGCTGATCCAACTTCAATTCTT	545	Db
6461	GGATTCGTTAAAGGTGATCAGCTGATCCAACTTCAATTCTT	6520	Qy
546	CTACCGTTTCTACACCCTTAAAATGCACTTAACTATTCCTGGATTCTAC	605	Db
6521	CTACCGTTTCTACACCCTTAAAATGCACTTAACTATTCCTGGATTCTAC	6580	Db
606	TATATATGGTAATCTCGCTTGCAGTTCTAGCTTAACTGATTAATCTAC	665	Db
6581	TATATATGGTAATCTCGCTTGCAGTTCTAGCTTAACTGATTAATCTAC	6640	Qy
666	TTTACTTTAAAGTGSAAATAGAGTCCTCTAGAGTTCAAGATGCC	725	Db
6641	TTTACTTTAAAGTGSAAATAGAGTCCTCTAGAGTTCAAGATGCC	6700	Qy
726	CITACTCTGACATCAATTGAGATTCAAGGGACTCTCTAGTTCACT	785	Db
6701	CITACTCTGACATCAATTGAGATTCAAGGGACTCTCTAGTTCACT	6760	Qy
786	GATTGCTGGTAGCCCTCTAGCTAAGGGACTCTCTAGTTCACT	845	Db
6761	GATTGCTGGTAGCCCTCTAGCTAAGGGACTCTCTAGTTCACT	6720	Qy
846	TACAGCCTAAAGATAAGATGAAATCTAGCAAGGGAGAGTTCATGG	905	Db
6821	TACAGCCTAAAGATAAGATGAAATCTAGCAAGGGAGAGTTCATGG	6880	Qy
906	GGAGAGTCCAAAGTGAGATTCCTGTTCTCCAGTGTCTGGCAAAGCA	965	Db
6881	GGAGAGTCCAAAGTGAGATTCCTGTTCTCCAGTGTCTGGCAAAGCA	6940	Qy
966	ATCTTCCTACATAAACTGTTGATAATTCAGTTCTGTTCTCCAGTGT	1025	Db
6941	ATCTTCCTACATAAACTGTTGATAATTCAGTTCTGTTCTCCAGTGT	7000	Qy
1026	TGAGCCCTGATTATATTGGAGCTTGGTCTGACAGATGTGACCTCTCAT	1085	Db
7001	TGAGCCCTGATTATATTGGAGCTTGGTCTGACAGATGTGACCTCTCAT	7060	Qy
1086	CTTCTAGTACTAGCCCTCCAGACGCTACAGCTTGGTCTGACAGATGT	1145	Db
7061	CTTCTAGTACTAGCCCTCCAGACGCTACAGCTTGGTCTGACAGATGT	7120	Qy
1146	CATAATACATCTGTAGACTCCAGTGAACTTCAACCTGTTACAGG	1205	Db
7121	CATAATACATCTGTAGACTCCAGTGAACTTCAACCTGTTACAGG	7180	Qy
1206	CTAAACGGCAGGATTTCAAAAGCTTAGGATGACTCCAGGCTGAATG	1265	Db
7181	CTAAACGGCAGGATTTCAAAAGCTTAGGATGACTCCAGGCTGAATG	7240	Qy
1266	CTCTGGCTCTTGGCAAGGAAATCTCTTACCGCACACTCTGCTCTG	1325	Db
7241	CTCTGGCTCTTGGCAAGGAAATCTCTTACCGCACACTCTGCTCTG	7300	Qy
1326	GAGGATCAAATGCTCATCTGCTGAGACCCGACATCTGCTCTG	1385	Db
7301	GAGGATCAAATGCTGCTGAGACCCGACATCTGCTCTGCTCTG	7360	Qy
1386	TCTCTATGTTGTTAACCTTGTGAGCTGCTGAAGACTTAAAGCTG	1445	Db
7361	TCTCTATGTTGTTAACCTTGTGAGCTGCTGAAGACTTAAAGCTG	7420	Qy
1446	ACAGATGGTCATTTAATCTCTCAAACTGGCTACAGGGACTCTG	1505	Db
7421	ACAGATGGTCATTTAATCTCTCAAACTGGCTACAGGGACTCTG	7480	Qy
1506	ACAGAGAAAGGACTGTGGATAAGAGGGTGGACCATGGTGGGATC	1565	Db

Db	181	GCTGAGTGCTAAGAAAGTTAGGCATGGCTTCACTGACTCACAGATGCTCATCTAAC	240	DT	23-NOV-1999	(first entry)
Qy	1465	TCAACAAATGGCTAACGGTGGCACTACTAGCCTCATTTGACAGGAAAGGACTGG	1524	XX	XX	hKuK2 enhancer of construct CN390.
Db	241	TCAACAAATGGCTAACGGTGGCACTACTAGCCTCATTTGACAGGAAAGGACTGG	300	DE	XX	prostate; cancer; drug assay; drug development; enhancer; promoter; tumour; kallikrein; androgen regulation; prostate specific antigen; construct; ss.
Qy	1525	ATAAGAGGGGTGACCAATAGGTCAGAGTCATTCTGATGCAAGGGCTCCAGAGCC	1584	KW	XX	
Db	301	ATAAGAGGGGTGACCAATAGGTCAGAGTCATTCTGATGCAAGGGCTCCAGAGCC	360	KW	XX	
Qy	1585	ATGATAGACAATGTCAGAGAAATTATGGCTGAATGCTCCTCCAGGGAAANGGGAA	1644	OS	XX	Synthetic.
Db	361	ATGATAGACAATGTCAGAGAAATTATGGCTGAATGCTCCTCCAGGGAAANGGGAA	420	PN	XX	Homo sapiens.
Qy	1645	TGCACPTTCCCTGACCCCTATCTGACATCTGACTTGGGTTATCTGACTCTCTCT	1704	PD	XX	W0941413-A2.
Db	421	TGCACPTTCCCTGACCCCTATCTGACATCTGACTTGGGTTATCTGACTCTCTCT	480	PF	XX	19-AUG-1999.
Qy	1705	ATGATACAGGAAAGCCATCAATACTCTCTCTGCTCTCCCTCGTCTTACTGC	1764	PR	XX	11-FEB-1999;
Db	481	ATGATACAGGAAAGCCATCAATACTCTCTCTGCTCTCCCTCGTCTTACTGC	540	PA	XX	99WO-US003117.
Qy	1765	CCACTCTCCCAGCTCATCCAGTGGCAGENGTAAGCTTAACTTAACTTTC	1824	PI	XX	(CALY-) CALYDON INC.
Db	541	CCACTCTCCCAGCTCATCCAGTGGCAGENGTAAGCTTAACTTAACTTTC	600	XX	XX	Henderson DR, Lamparski HG, Schuur ER, Yu DC;
Qy	1825	AGAGAACTTAAATGCTGTTATCTACAGGGAGAAAAAAAAGACTCTGAAGAGCTG	1884	PT	XX	WPI; 1999-527378/44.
Db	601	AGAGAACTTAAATGCTGTTATCTACAGGGAGAAAAAAAAGACTCTGAAGAGCTG	660	PT	XX	Screening for compounds which inhibit prostate cancer using a cell line containing a marker whose expression is responsive to therapeutically active compounds.
Qy	1885	ACATTTACCACTTCCAAACATAAGCTTACCTGCACTGCACTGCAACTCA	1944	XX	XX	Claim 6; Page 49; 50DP; English.
Db	661	ACATTTACCACTTCCAAACATAAGCTTACCTGCACTGCACTGCAACTCA	720	CC	XX	This is the nucleotide sequence of the hKuK2 enhancer region contained in construct CN390. hKuK2 is a member of the kallikrein family, as is the prostate specific antigen (PSA), a chymoeruptin-like protein that is synthesized exclusively by normal, hyperplastic, and malignant prostatic epithelia. This tissue specific nature of PSA makes it an excellent biomarker for identifying benign prostatic hyperplasia (BPH) and prostate carcinoma (Cap). Elevated levels of PSA are indicative of BPH or Cap. Like PSA, hKuK2 is expressed exclusively in the prostate and is up-regulated by androgens, primarily by transcription activation. The proteins also exhibit a high degree of amino acid sequence identity and contain similar regulatory elements. The characterisation of genes whose expression is limited to the prostate allows the development of screening methods which can identify substances capable of specifically altering the expression of prostate-specific genes.
Db	1945	TGAGACUCCTGGTCAAGGGAAAGAGTTTATTACCAAGCTTAAGGGAGCATGAA	2004	CC	XX	Sequence 1172 BP; 334 A; 257 C; 268 G; 313 T; 0 U; 0 Other;
Db	721	TGAGACTCTCTGGTCAAGGGAAAGATTTATTACCAAGCTTAAGGGAGCATGAA	780	CC	XX	Query Match Score 1172; DB 2; Length 1172;
Qy	2005	CTTGTGTCTCACATTGTTCACTTGCCTCCCTCAATCTGGATGATCAGGCACTTC	2064	Best Local Similarity 10.0%; Pred. No. 0;	0	Best Local Similarity 10.0%; Pred. No. 0;
Db	781	CTTGTGTCTCACATTGTTCACTTGCCTCCCTCAATCTGGATGATCAGGCACTTC	B40	Mismatches 0;	0	Mismatches 0;
Qy	2065	AGGTGGATGGCACACGGGTTGTGGCAAAAGTGCAACCTAGGCTTAGAAATCCTCAA	2124	Db	1172	Conservative
Db	841	AGGTGGATGGCACACGGGTTGTGGCAAAAGTGCAACCTAGGCTTAGAAATCCTCAA	900	Qy	1225	Matched
Qy	2125	TCTTATAAGGGTACTAGGCAACTTCACTGCAACTTCACTGCTGATCTGAGGAGATAATTCT	2184	Db	1225	CAAAGCTTAGAGCTGACCTCCAGGAGCTTAATGCAAAAGACCTGGCCTTTGGCGAAG
Db	901	TCTTATAAGGGTACTAGGCAACTTCACTGCAACTTCACTGCTGATCTGAGGAGATAATTCT	960	Qy	1225	1
Qy	2185	TATAATTGGTGAAGCAGACCTACTCTGAGGACATAATTGCTGTTCTGAAAC	2244	Db	1225	CAGAGCTTCTTACGGCAACTCTCTCCTCACGGGTTATTGGAGGATCAATGTGCTCAT
Db	961	TATAATTGGTGAAGCAGACCTACTCTGAGGACATAATTGCTGTTCTGAAAC	1020	Qy	1225	1080
Qy	2245	AGTAACAAATCTGCTGAAATAAGCGTTAACCTTAACTGCAAGCTAACACC	2304	Db	1225	1080
Db	1021	AGTAACAAATCTGCTGAAATAAGCGTTAACCTGCTGAAAC	1080	Qy	1225	1080
Qy	2305	TAGATCTGAAGGGATAACCACCTTGGCAAGGCTATCTGCTGAAATAATGCTGAAAGA	2364	Db	1225	1080
Db	1081	TAGATCTGAAGGGATAACCACCTTGGCAAGGCTATCTGCTGAAATAATGCTGAAAGA	1140	Qy	1225	1080
Qy	2365	TGGTCCAAGAAAAGAACGGTTATTGCTT	2396	Db	1225	1080
Db	1141	TGGTCCAAGAAAAGAACGGTTATTGCTT	1172	Qy	1225	1080
Db	181	GCAGAGCTGCTAAGAAATATTGGCTGCTAAGAACTCACTGAGCTATCPATCC	240	Qy	1225	1080
Qy	1465	TCAAAACATGGCTACAGGTGGCAACTACTAGCCCTCATTTGAGGAGCTGTTGG	1524	Db	1225	1080
Db	241	TCAAAACATGGCTACAGGTGGCAACTACTAGCCCTCATTTGAGGAGCTGTTGG	300	Qy	1225	1080
Qy	1525	ATAGAGGGGGTGACCAATAGGTCAAGGACCTGCTGAAAGGACCTGAGGACCT	1584	XX	RESULT 11	
AAZ06494				ID	AAZ06494	standard; DNA; 1172 BP.
XX				XX		
AC				AC	AAZ06494;	
XX				XX		

Qy	1424	TAGGGATGGCTTCAGCACTCACAGATGGTCATCTATACTCTCACAACTGGCTACAGG	1483		Db	1439	CATTAGTGTGCTTACCGTGCCTAACATCTGGCTTACCGTGCCTAACAGGTTCTAGGTCAAGTT	1498
Db	360	TAGGGATGGCTTCAGCACTCACAGATGGTCATCTATACTCTCACAACTGGCTACAGG	419		Qy	1484	CCGCCCATGTTGGAGTGGCTGCGCCACTGCCAACCCGAATAAGGGAGTGTAGAATTTCAGAATTTC	2623
Oy	1484	TGGGCACTACTAGCCTCATTGGACAGGAAGGACTGTGATTAAGAACGGGTGACCAA	1543		Db	1499	CCGCCCATGTTGGAGTGGCTGCGCCACTGCCAACCCGAATAAGGGAGTGTAGAATTTCAGAATTTC	1558
Db	420	TGGGCACTACTAGCCTCATTGGACAGGAAGGACTGTGATTAAGAACGGGTGACCAA	479					
Qy	1544	TAGGGCACTGATTGGATGGCAAGGGGTCCAGAGACCATGATTAGACATTTGGTCG	1603					
Db	480	TAGGTAGAGTCATTGGATGGTCAGGGTCCAGAGACATTTAGACATTGTCG	539					
Oy	1604	AGAGAAATTATGGCTGGATCTCTCNGCCGGAAAGGGGATGACTTCCTGACCCC	1663					
Db	540	AGAGAAATTATGGCTGGATCTCTCNGCCGGAAAGGGGATGACTTCCTGACCCC	599					
Qy	1664	TATCTGATCTTGACTTGAGGTATCTAGACCTCTCTGATATACTGATA	1723					
Db	600	TATCTGAGATTTGAGTTGACTTGAGGTATCTAGACCTCTGATA	659					
Qy	1724	ATAATCTCTCTGTCCTCCCTCTCAGCTCTAGCTCTCCACTCTCCAGCTC	1783					
Db	660	ATAATCTCTCTGTCCTCCCTCTCAGCTCTAGCTCTCCACTCTCCAGCTC	719					
Oy	1784	CTCCAGCTGGCAGGGTAGCCAGTACCTGACCTAACTCTGAGCTTAATGTTA	1843					
Db	720	CTCCAGCTGGCAGGGTAGCCAGTACCTGACCTAACTCTGAGCTTAATGTTA	779					
Qy	1844	TCCTACAGGGAGAAAAAAAAGAACTCTGAAAGAGCTGACATTTCACCGACTTC	1903					
Db	780	TCCTACAGGGAGAAAAAAAAGAACTCTGAAAGGCTGACATTTCACCGACTTC	838					
Oy	1904	ACACATAAGCTAACCTGCCGTTTGTGCTGGTACAACCTCATGAGACTCTGGCTC	1963					
Db	839	ACACATAAGCTAACCTGCCGTTTGTGCTGGTACAACCTCATGAGACTCTGGCTC	898					
Oy	1964	GCAAAAGATTTTATACCAAGCTAAAGGAGAACATGAGCTTGTGTTCAATTGTT	2023					
Db	899	GCAAAAGATTTTATACCAAGCTAAAGGAGAACATGAGCTTGTGTTCAATTGTT	958					
Qy	2024	CACTTGGCCCCAATTATCATATGGGATGATGAGGGAGTACAGGGAG	2083					
Db	959	CACTTGGCCCCAATTATCATATGGGATGATGAGGGAGTACAGGGAG	1018					
Qy	2084	TGTGGCGCAAGGTGAGCAACCTAGGCTTAACTTAAAGGTTACTAG	2143					
Db	1019	TGTGGCGCAAGGTGAGCAACCTAGGCTTAACTTAAAGGTTACTAG	1078					
Qy	2144	CAAACTGTCCAGTCTGGAGACATATTGTATCTGAGGAGATAATTGGTCAAGCA	2203					
Db	1079	CAAACTGTCCAGTCTGGAGACATATTGTATCTGAGGAGATAATTGGTCAAGCA	1138					
Qy	2204	GACCTACTCTGGAGAACATATTGTATCTGAGGAGATAATTGGTCAAGCA	2263					
Db	1139	GACCTACTCTGGAGAACATATTGTATCTGAGGAGATAATTGGTCAAGCA	1198					
Qy	2264	AAATAGCGTTAACCTTATCTGAGCTAGAACCTGAGATCTGAGGGATACC	2323					
Db	1199	AAATAGCGTTAACCTTATCTGAGCTAGAACCTGAGATCTGAGGGATACC	1258					
Oy	2324	ATCTTGAAAGGCTTATCTGCTGACAAATATGCTTAACTGAGCTTAACTCCCAT	2383					
Db	1259	ATCTTGAAAGGCTTATCTGCTGACAAATATGCTTAACTGAGCTTAACTCCCAT	1318					
Qy	2384	GTATTATGCTTTCAGAGACAGAACATAGAAACCATGAAATTGGCT	2443					
Db	1319	GTATTATGCTTTCAGAGACAGAACATAGAAACCATGAAATTGGCT	1378					
Oy	2444	CCAAACACTGTTCACCGAACCTCTGCTGAGCTTAACTCCCAT	2503					
Db	1379	CCAAACACTGTTCACCGAACCTCTGCTGAGCTTAACTCCCAT	1438					
Oy	2504	CATTAGTGTGCTTACCACTGCTTACCGTGCCTAACAAATTCTAGGTCAAGT	2563					

Db	1 CAAAGCTTAGAGATGACCTCCCAGGGCTGAATGCAAAGACCTGGCTCTGGCAAG 60	DT XX	21-JUN-1999 (first entry)
Qy	1285 GAGAATCCTAACGGACACTCCCTCACGGTATTTGAGGATCAATGGGTAT 1344	DE XX	Human glandular kallikrein hKLU2 gene enhancer with mutated ARE.
Db	61 GAGAATCCTAACGGACACTCCCTCACGGTATTTGAGGATCAATGGGTAT 120	XX	Enhancer; glandular kallikrein-1; hKLU2; human; prostate cancer;
Qy	1345 GTGTGTGAGACACCACATGGCTGGCTGGACAGTCACTTGTTGCTAACTT 1404	KW XX	therapy; androgen response element; mutant; ss.
Db	121 GTGTGTGAGACACCACATGGCTGGCTGGACAGTCACTTGTTGCTAACTT 180	OS XX	Homo sapiens.
Db	181 GCTGAGTGTGAGAAAGTATTAGGCATGGCTTCAGCACTCACATACTTC 1464	Synthetic. XX	
Qy	1405 GCTGAGTGTGAGAAAGTATTAGGCATGGCTTCAGCACTCACATACTTC 240	Key FT	Location/Qualifiers mutation replace (93..100/ GTACTATATACAGT)
Db		PH FT	/tag= a /note= "mutated androgen response element"
Qy	1465 TCACACATGGCTAACGGGGCACTACTAGCCTCATTTGAGGAAAGGACTGTG 1524	XX	
Db	241 TCACACATGGCTAACGGGGCACTACTAGCCTCATTTGAGGAAAGGACTGTG 300	PN XX	WO9906576-A1.
Qy	1525 ATAAGGAGGGGTGACCATTAAGGTAGTAGTCATCTGGATGCAAGGGCTCCAGAGGC 1584	PD XX	11-FEB-1999.
Db	301 ATAAGGAGGGGTGACCATTAAGGTAGTAGTCATCTGGATGCAAGGGCTCCAGAGGC 360	PF XX	04-AUG-1998; 98WO-US016312.
Qy	1585 ATGATTAGACATTGTGTGAGAAATTAGGTGAGTCATCTGGATGCAAGGGCTCCAGAGGC 1644	PR XX	04-AUG-1997; 97US-0051523P.
Db	361 ATGATTAGACATTGTGTGAGAAATTAGGTGAGTCATCTGGATGCAAGGGCTCCAGAGGC 420	PT XX	02-MAR-1998; 98US-007545P.
Qy	1645 TGCACTTCCCTGACCCCTATCTGAGCTTGAGTTATCTGAGCTTCCCTCT 1704	PS XX	03-AUG-1998; 98US-00127834.
Db	421 TGCACTTCCCTGACCCCTATCTGAGCTTGAGTTATCTGAGCTTCCCTCT 480	PA XX	(CALLY) CALYDON INC.
Qy	1705 ATGATACCGAGGCCATATAATCTCTGTCCTCCCCCTTCAGCTTACTGC 1764	PI XX	Yu D., Herdenson DR, Schuur ER;
Db	481 ATGATACCGAGGCCATATAATCTCTGTCCTCCCCCTTCAGCTTACTGC 540	DR XX	WPI: 1999-153804/13.
Qy	1765 CCACCTTCCCAAGCTCCATCCAGCTGGCAAGGTGACCCAGACTCTCTGC 1824	PT XX	New nucleic acid containing the human glandular kallikrein enhancer -
Db	541 CCACCTTCCCAAGCTCCATCCAGCTGGCAAGGTGACCCAGACTCTCTGC 600	PT XX	providing increased expression of heterologous sequences in prostatic cells, and related adenoviral vectors for treating prostatic cancer.
Qy	1825 AGAGACTATAATTGTATCTAACGGGAGAAAAAAAGAACCTGAAAGCTG 1884	PS XX	Example 7; Page 169; 179pp; English.
Db	601 AGAGACTATAATTGTATCTAACGGGAGAAAAAAAGAACCTGAAAGCTG 660	XX	This polynucleotide is based on nucleotides 7200-8371 of the 5' flanking region of the Human Glandular kallikrein (hKLU2) gene (see AX24755), the putative androgen response element (ARE) of the native sequence (see AX24772) has been mutated. This mutation was shown to affect the enhancer function of this region of the hKLU2 gene. hKLU2 enhancers of the invention have been shown to increase the transcription of cis-linked coding sequences in prostate cells. Methods of using DNA constructs comprising the enhancers to control transcription of heterologous polynucleotides are provided. Adenoviral vectors in which one or more genes are under transcriptional control of a hKLU2 transcription regulatory element are claimed, and can be used to confer selective cytotoxicity in mammalian cells for use e.g. in the treatment of prostate cancer
Qy	1885 ACATTTCACCGACTGCAACACATAAGCTTAACCTGGCAAGGTGACCCAGACTCTCTGC 1944	SQ Sequence 1172 BP; 334 A; 258 C; 267 G; 313 T; 0 U; 0 Other;	Sequence 1172 BP; 334 A; 258 C; 267 G; 313 T; 0 U; 0 Other;
Db	661 ACATTTCACCGACTGCAACACATAAGCTTAACCTGGCAAGGTGACCCAGACTCTCTGC 720	Query Match 27.2%; Score 993; DB 2; Length 1172;	Query Match 27.2%; Score 993; DB 2; Length 1172;
Qy	1945 TGAGACTCTGGCTAACGGCAALAGATTATTACCCACGCTAACGGAGCATGA 2004	Best Local Similarity 100.0%; Prod. No. 0;	Best Local Similarity 100.0%; Prod. No. 0;
Db	721 TGAGACTCTGGCTAACGGCAALAGATTATTACCCACGCTAACGGAGCATGA 780	Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2005 CTTGTGTTACATTGTTCACTTGGCCCCATTCAATGGATGATGAGCAGTC 2064	Qy 1225 CAAAGCTTAGAGTAGCTCCAGGAGCTGGCTCTGGCAG 1284	
Db	781 CTTGTGTTACATTGTTCACTTGGCCCCATTCAATGGATGATGAGCAGTC 840	Db 1 CAAAGCTTAGAGTAGCTCCAGGAGCTGGCTCTGGCAG 60	
Qy	2065 AGGTGATGACACAGGGTTGGCAAGGGACCTAGGCTTAAGATCTCA 2124	Qy 1285 GAGATCCTTACCCACACTCTCTCAAGGTTATGTGGATCAAATGTGCAT 1344	
Db	841 AGGTGATGACACAGGGTTGGCAAGGGACCTAGGCTTAAGATCTCA 900	Db 61 GAGATCCTTACCCACACTCTCTCAAGGTTATGTGGATCAAATGTGCAT 120	
Qy	2125 TCTTATAAGGGTACTAGAAAATTGTCACTTGTGTTGGCAAGGATATTCT 2184	Qy 1345 GTGTGTGAGACCCAGCAATGTGGCTGTGGAGAGTGAACCTCTATGTGTGTAATT 1404	
Db	901 TCTTATAAGGGTACTAGAAAATTGTCACTTGTGTTGGCAAGGATATTCT 960	Db 121 GTGTGTGAGACCCAGCAATGTGGCTGTGGAGAGTGAACCTCTATGTGTGTAATT 180	
Qy	2185 TATAATTGGTTGAAAGCAACCTCTGGAG 2217	Qy 1405 GCTGAGTGTGAAAGAAGTATTAGGCATGGCTTCAAGATGCTCATCTATCC 1464	
Db	961 TATAATTGGTTGAAAGCAACCTCTGGAG 993	Db 181 GCTGAGTGTGAAAGAAGTATTAGGCATGGCTTCAAGATGCTCATCTATCC 240	
RESULT 14			
AAK4773			
ID AAK4773 standard: DNA; 1172 BP.			
XX			
AC AAK4773:			
XX			

Qy	1465	TCAACAGATGGCTACAGGGGGGACACTAGCCCATTTGACAGAGGAAGGACTGTGG	1524	XX	11-FEB-1999;	99WC-US003117.	
Db	241	TCAACAGATGGCTACAGGGGGGACACTAGCCCATTTGACAGAGGAAGGACTGTGG	300	PF	12-FEB-1998;	98US-00022732.	
Qy	1525	ATAAGAAGGGGGTGCACAAATTAGGTCAGAGTCATTCGGATGCAAGGGGCTCAGAGGCC	1584	XX	(CAYL-Y) CALYDON INC.		
Db	301	ATAAGAAGGGGGTGCACAAATTAGGTCAGAGTCATTCGGATGCAAGGGGCTCAGAGGCC	360	PA	Henderson DR, Lamparski HG, Schaurr ER, Yu DC;		
Qy	1585	ATGATTA GACATTGTTGTCAGAGAAATTATGGTGGATTCCTGCCCCGAAAGGGGA	1644	XX	WPI : 1999-527378/44.		
Db	361	ATGATTA GACATTGTTGTCAGAGAAATTATGGTGGATTCCTGCCCCGAAAGGGGA	420	XX	Screening for compounds which inhibit prostate cancer using a cell line containing a marker whose expression is responsive to therapeutically active compounds.		
Qy	1645	TGCACATTTCCTTGACGCCCPATCAGATCTGACTTGGGTTATCGACTCTCTCT	1704	PT	PS Claim 6; Page 50; 50pp; English.		
Db	421	TGCACATTTCCTTGACGCCCPATCAGATCTGACTTGGGTTATCGACTCTCTCT	480	XX	This is the nucleotide sequence of the hKLK2 enhancer region contained in construct CN457. hKLK2 is a member of the kallikrein family, as is the prostate specific antigen (PSA), a chymotrypsin like protein that is synthesized exclusively by normal, hyperplastic, and malignant prostatic epithelia. This tissue specific nature of PSA makes it an excellent biomarker for identifying benign prostatic hyperplasia (BPH) and prostate carcinoma (Cap). Elevated levels of PSA are indicative of BPH or Cap. Like PSA, hKLK2 is expressed exclusively in the prostate and is up regulated by androgens, primarily by transcription activation. The proteins also exhibit a high degree of amino acid sequence identity and contain similar regulatory elements. The characterisation of genes whose expression is limited to the prostate allows the development of screening methods which can identify substances capable of specifically altering the expression of prostate-specific genes.		
Qy	1705	ATGATCACAGGGCCATCATATACTCTCTGTCCTCTCCCTGCTACTGTTAC TGC	1764	SQ	Sequence 1172 BP; 334 A; 258 C; 267 G; 313 T; 0 U; 0 Other;		
Db	481	ATGATCACAGGGCCATCATATACTCTCTGTCCTCTCCCTGCTACTGTTAC TGC	540	Query Match Score 993; DB 2; Length 1172;			
Qy	1765	CCACTTCCAGCTCCATTCACATCCACCTGGCAGGTGACCTAACCTCTTGC	1824	CC	Best Local Similarity 100.0%; Pred. No. 0;		
Db	541	CCACTTCCAGCTCCATTCACATCCACCTGGCAGGTGACCTAACCTCTTGC	600	Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1825	AGAGAACTATAATGGTATCTACAGGGAGAAAAAAAGACTCTGAAGAGCTG	1884	CC	CC		
Db	601	AGAGAACTATAATGGTATCTACAGGGAGAAAAAAAGACTCTGAAGAGCTG	660	CC	CC		
Qy	1885	ACATTATACCGACTTTGCAAACATAAGCTAACCTGCAGTTTGTGCTGGTAAACTCA	1944	CC	CC		
Db	661	ACATTATACCGACTTTGCAAACATAAGCTAACCTGCAGTTTGTGCTGGTAAACTCA	720	XX	CC		
Qy	1945	TGAGACTCTGGCTAGAGGCAAAAGATTTTATPACCCACAGCTAACAGTAAGGGGCCATCAA	2004	SQ	Sequence 1172 BP; 334 A; 258 C; 267 G; 313 T; 0 U; 0 Other;		
Db	721	TGAGACTCTGGCTAGAGGCAAAAGATTTTATPACCCACAGCTAACAGTAAGGGGCCATCAA	780	Query Match Score 993; DB 1; Length 1172;			
Qy	2005	CTTTGTGTTTCAATTGTTTACTTGGATGATGAGCAGTC	2064	CC	Best Local Similarity 100.0%; Pred. No. 0;		
Db	781	CTTTGTGTTTCAATTGTTTACTTGGATGATGAGCAGTC	840	Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2065	AGGTGGATGGACACAGGGTTGGCAAGGTGACACTGGCTTAGAAATCCTCAA	2124	QY	1225 CAAAAGCTTAGAGTACCTCCAGAGCTTAATGGCAAGCTCTTGGCCAAG	1284	
Db	841	AGGTGGATGGACACAGGGTTGGCAAGGTGACACTGGCTTAGAAATCCTCAA	900	DB	1 CAAAAGCTTAGAGTACCTCCAGAGCTTAATGGCAAGCTCTTGGCCAAG	60	
Qy	2125	TCTTATAAGGGTACTACGAAACTGTCCAGTCTTGTATCTGACGGAGATATTCTT	2184	QY	1285 GAGAATCTTACCGCAGACTCTCCTCACGGGTATTGTGAGCATAAATGGTCT	1344	
Db	901	TCTTATAAGGGTACTACGAAACTGTCCAGTCTGACGGAGATATTCTT	960	DB	61 GAGAATCTTACCGCAGACTCTCCTCACGGGTATTGTGAGCATAAATGGTCT	120	
Qy	2185	TATAATTGGGTTGAAAGCAGACCTACTCTGGG	2217	QY	1345 GTGTGTGAGCACAGGAGACATGCTGGCTGGAGAGTGACTCTATGTGCTACATT	1404	
Db	961	TATAATTGGGTTGAAAGCAGACCTACTCTGGG	993	DB	121 GTGTGTGAGCACAGGAGACATGCTGGCTGGAGAGTGACTCTATGTGCTACATT	180	
Qy	2217	GTGTGTGAGCACAGGAGACATGCTGGCTGGAGAGTGACTCTATGTGCTACATT	1464	QY	1405 GTGTGTGCTAAAGAACTTAAAGCATGGCTTCAAGCACTACAGATGCTCATTAATCC	1464	
Db	993	GTGTGTGAGCACAGGAGACATGCTGGCTGGAGAGTGACTCTATGTGCTACATT	1464	DB	181 GTGTGTGCTAAAGAGTATTAGGATGGCTTCAAGCACTACAGATGCTCATTAATCC	240	
Qy	1465	TCACACATGGCTACAGGTGGGACTACTAGCCATTTGAGCATTCAGGCTTCAAGGGCTCCAGGGACC	1524	QY	1525 ATAAAGAAGGGGTGACCAATGGCTGAGGAAATTATGGCTGATGTCTGGATGCTCATTCATTC	1584	
Db	241	TCACACATGGCTACAGGTGGGACTACTAGCCATTTGAGCATTCAGGCTTCAAGGGCTCCAGGGACC	300	DB	301 ATAAAGAAGGGGTGACCAATGGCTGAGGAAATTATGGCTGATGTCTGGATGCTCATTCATTC	360	
Qy	1585	ATGATTAGACATGTCTGAGAAATTATGGCTGATGTCTGGATGCTCATTCATTC	1644	QY	1585 ATGATTAGACATGTCTGAGAAATTATGGCTGATGTCTGGATGCTCATTCATTC	1644	
Db	361	ATGATTAGACATGTCTGAGAAATTATGGCTGATGTCTGGATGCTCATTCATTC	420	DB	361 ATGATTAGACATGTCTGAGAAATTATGGCTGATGTCTGGATGCTCATTCATTC	420	
Qy	1645	TGCACATTTCCTGACGCCCATATCTGAGCTTCAAGCTTCAAGATCTGAGACTCTCT	1704	QY	1645 TGCACATTTCCTGACGCCCATATCTGAGCTTCAAGCTTCAAGATCTGAGACTCTCT	1704	
Db	421	TGCACATTTCCTGACGCCCATATCTGAGCTTCAAGCTTCAAGATCTGAGACTCTCT	480	DB	421 TGCACATTTCCTGACGCCCATATCTGAGCTTCAAGCTTCAAGATCTGAGACTCTCT	480	
Qy	1705	ATGATACAGGGCCATCATTAATCTGCTGGCTCTCCCTGCTCATTCAGACTCTCT	1764	QY	1705 ATGATACAGGGCCATCATTAATCTGCTGGCTCTCCCTGCTCATTCAGACTCTCT	1764	
Db	481	ATGATACAGGGCCATCATTAATCTGCTGGCTCTCCCTGCTCATTCAGACTCTCT	540	DB	481 ATGATACAGGGCCATCATTAATCTGCTGGCTCTCCCTGCTCATTCAGACTCTCT	540	

RESULT 15

AAZ06495 standard; DNA; 1172 BP.
ID AAZ06495

AAZ06495;

XX DT 23-NOV-1999 (first entry)

XX DE hKLK2 enhancer of construct CN457.

XX KW prostate; cancer; drug assay; drug development; enhancer; promoter; tumour; kallikrein; androgen regulation; prostate specific antigen; construct; ss.

XX OS Synthetic.

OS Homo sapiens.

XX PN W09911413-A2.

XX PD 19-AUG-1999.

Qy	1765	CCACCTTCCAGTCATCTCCAGCTGCCAGTGAACTCCACTCTTG	1824	prostate specific antigen (PSA), a chymotrypsin like protein that is synthesized exclusively by normal, hyperplastic and malignant prostate epithelia. This tissue specific nature of PSA makes it an excellent biomarker for identifying benign prostatic hyperplasia (BPH) and prostatic carcinoma (Cap).
Db	541	CCACCTTCCAGCTCCATCTCCAGCTGCCAGTGAACTCCACTCTTG	600	or Cap. Like PSA, hKLK2 is expressed exclusively in the prostate and is up regulated by androgens, primarily by transcription activation. The proteins also exhibit a high degree of amino acid sequence identity and contain similar regulatory elements. The characterisation of genes whose expression is limited to the prostate allows the development of screening methods which can identify substances capable of specifically altering the expression of prostate-specific genes.
Qy	1825	AGAGACTATAATGTGATCCTACGGAGAAAAAAAARGAACCTG	1884	Sequence 1172 BP: 335 A; 258 C; 268 G; 311 T; 0 U; 0 Other;
Db	601	AGAGACTATAATGTGATCCTACGGAGAAAAAAAARGAACCTG	660	Query Match 27.2%; Score 993; DB 2; Length 1172;
Qy	1885	ACATTAACTGCAAAACATAAGCTAACATGCGAGTTGTGCTG	1944	Best Local Similarity 100.0%; Pred. No. 0;
Db	661	ACATTAACTGCAAAACATAAGCTAACATGCGAGTTGTGCTG	720	Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1945	TGAGACTCTGGTCAGAGGCAAAGATTTAATACCCACGCTAAGG	2004	Qy 1225 CAAAAGCTTAGAGATGACCTCTGGCTCCAGAGCTGAATGCAARGACCTGGCTCTGGCZAG 1284
Db	721	TGAGACTCTGGTCAGAGCAGATTTAACCCACGCTAAGG	780	Db 1 CAAAGCTTAGAGATGACCTCTGGCTCCAGAGCTGAATGCAARGACCTGGCTCTGGCZAG 60
Qy	2005	CTTGTGTTACATTTGTGACTTTGCCCAATTCTATGGATCATGAGCA	2064	Qy 1285 GAGATATCTTACCGCACACTCTCTCACAGGTTATGTGAGGATCAATGTGCTGAT 1344
Db	781	CTTGTGTTACATTTGTGACTTTGCCCAATTCTATGGATCATGAGCA	840	Db 61 GAGAACTCTTACCGCACACTCTCTCACAGGTTATGTGAGGATCAATGTGCTGAT 120
Qy	2065	AGGTGATGACACAGCACATGTCAGTGGCAAGGTAGCAGCTTA	2124	Qy 1345 GTGTGAGACACCAGCACATGTCAGTGGAGAGTGACTCTATGTGCTGCTAACATT 1404
Db	841	AGGTGATGACACAGGGTTGTGCAAGGTAGCAGCACTTAGGCTTA	900	Db 121 GTGTGAGACACCAGCACATGTCAGTGGAGAGTGACTCTATGTGCTGCTAACATT 180
Qy	2125	TCTTTAAAGAGGTACTAGCAAACCTGTGAGTCTGACGSSGATA	2184	Qy 1405 GCTGACTCTGGTAAGAGAGTATTAGGATCTGAGCTCACATCTAATCC 1464
Db	901	TCTTTAAAGAGGTACTAGCAAACCTGTGAGTCTGACGSSGATA	960	Db 181 GCTGACTCTGGTAAGAGAGTATTAGGATCTGAGCTCACATCTAATCC 240
Qy	2185	TATAATTGGTTGAAAGCAGACCTACTCTGGAG 2217		Qy 1465 TCACACATGGCTACAGGTGGCACTACTAGCTCTA 1524
Db	961	TATAATTGGTTGAAAGCAGACCTACTCTGGAG 993		Db 241 TCACACATGGCTACAGGTGGCACTACTAGCTCTA 300
<hr/>				
RESULT 16				Qy 1525 ATAAGAGGGGTGACAATAGGTGAGTCATCTGGTCAATTGAGAGGAACTGCG 1584
ID AAZ06496				Db 301 ATAGAGGGGTGACAATAGGTGAGTCATCTGGTCAATTGAGAGGAACTGCG 360
XX AAZ06496 standard				Qy 1585 ATGATTAGACATTGTCAGAGAAATTAGGCTGATCTGCCCCGAAAGGGGA 1644
XX				Db 361 ATGATTAGACATTGTCAGAGAAATTAGGCTGATCTGCCCCGAAAGGGGA 420
AC AAZ06496;				Db 421 TGCACTTCCCTGACCCCTATCTGAGCTTCTGACTTCTGACTTCTCT 480
DT 23-NOV-1999				Qy 1705 ATGATPACCTGGAGCCATATACTCTCTGAGCTTCTCTGAGCTTCTCTGC 1764
XX hKLK2 enhancer of construct CN458.				Db 481 ATGATPACCTGGAGCCATATACTCTGAGCTTCTCTGC 540
DE				Qy 1765 CCACPTTCCOAGCTCATACTCCAGCTGAGCCAGGTAGCCAGTAACTCTTG 1824
XX prostate; cancer; drug assay; drug development; enhancer; promoter;				Db 541 CCACPTTCCOAGCTCATACTCCAGCTGAGCCAGGTAGCCAGTAACTCTTG 600
KW tumour; Kallikrein; androgen; regulation; prostate specific antigen;				Qy 1825 AGAGAACTATAATGTGTATCCTAAGGGAGAAAAAAAGACTGTGAGGTG 1884
KW construct; ss.				Db 601 AGAGAACTATAATGTGTATCCTAAGGGAGAAAAAAAGACTGTGAGGTG 660
OS Synthetic.				Qy 1885 ACATTTACGGACTGCAACATAAGCTTAACCTGCTGAGTAACTGCA 1944
XX Homo sapiens.				Db 661 ACATTTACGGACTGCAACATAAGCTTAACCTGCTGAGTAACTGCA 780
PN WO931413-A2.				Qy 1945 TGAGACTCTGGGTCAAGGCAAAAGATTATTACCCACGCTAAGGAGCAGTAACTGCA 2004
XX				Db 721 TGAGATCTCCGGTGTACATTTGTCACCTGGCCAGTTGCTGAGTAACTGCA 780
PD 19-AUG-1999.				CC This is the nucleotide sequence of the hKLK2 enhancer region contained in construct CN458. hKLK2 is a member of the kallikrein family, as is the
XX				CC construct CN458.
PF 11-FEB-1999;				PS Claim 6; Page 50; 5opp; English.
XX				XX Screening for compounds which inhibit prostate cancer using a cell line containing a marker whose expression is responsive to therapeutically active compounds.
PR 12-FEB-1998;				XX
PA (CALY-) CALYDON INC.				XX
PI Henderson DR, Lamparski HG, Schuur ER, Yu DC;				XX
XX				XX
DR WPI: 1999-5227378/44.				XX
XX				XX
PT Screening for compounds which inhibit prostate cancer using a cell line				XX
PT containing a marker whose expression is responsive to therapeutically active compounds.				XX
XX				XX
PS				XX
XX				XX
CC				CC

Db 781 CTTTGTGTCACATTGGTCACTTGCCCCAATTCATATGGATGATCAGGAGTC 840
 Qy 2065 AGGTGGATGACAAGGGTTTGTGCAAGGTGAGCACTTAGGCTTAGAAATCTCAA 2124
 Db 841 AGGGGGATGGACAGGGGTTTGGCAAGGTGAGCACTTAGGCTTAGAAATCTCAA 900
 Qy 2125 TCTTATAAGGGTACTAGCAAATTGTGCAGTCTTGTATCTGACGGAGATATTCTT 2184
 Db 901 TCTTATAAGGGTACTAGCAAATTGTGCAGTCTTGTATCTGACGGAGATATTCTT 960
 Qy 2185 TATAATTGGTTGAAGGAGACCTACTCTGGAG 2217
 Db 961 TATAATTGGTTGAAGGAGACCTACTCTGGAG 993

RESULT 17
 AACF92694 standard; DNA; 204 BP.
 XX
 AACF92694;
 XX
 DT 18-JUN-2001 (first entry)
 DE Glandular HK2 enhancer core sequence.
 XX
 Androgen response element; ARE; cytostatic; gene therapy;
 prostate-specific chimeric enhancer; transcriptional regulation;
 targeted gene expression; prostate cancer; Prostate disorder;
 prostate specific antigen; PSA; glandular HK2; ds.
 KW Unidentified.
 OS WO200127256-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028444.
 XX
 PR 14-OCT-1999; 99US-0159691P.
 PR 15-OCT-1999; 99US-0159730P.
 XX
 PA (RESC) UNIV CALIFORNIA SYSTEM.
 XX
 PI Wu L, Carey MF, Belldegrun AS;
 XX
 DR WPI; 2001-273768/2B.
 XX
 New polynucleotide, useful for treating prostatic cancer, comprises
 prostate specific chimeric enhancer and proximal promoter sequence
 operably linked to nucleic acid encoding heterologous polypeptide.

Claim 17: Page 80; 131PD; English.

The present sequence may be used in an invention relating to an isolated polynucleotide comprising a prostate-specific chimeric enhancer (PSE) sequence and a proximal promoter sequence operably linked to a nucleic acid segment that encodes a heterologous polypeptide. The PSE contains an ARE and specifically activates transcription of the nucleic acid segment in a mammalian prostate cell. The construct is useful for the treatment of a prostate disorder or a metastasized prostate cancer, such as hyperplasia or hyperproliferation of prostate cells. It is also useful for directing the tissue-specific expression of a heterologous polypeptide in a human prostate cell. The construct may be administered by injection, infection, transformation, liposome-mediated transfection, polybrene-mediated transfection, receptor-mediated uptake or Ca-PG-mediated transformation.

Sequence 204 BP; 67 A; 34 C; 39 G; 64 T; 0 U; 0 Other;

Query Match 5.6%; Score 204; DB 5; Length 204;
 Best Local Similarity 100.0%; Pred. No. 7.9e-88;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: August 11, 2004 , 03:40:18
 Job time : 8672 secs

OM nucleic - nucleic search, using sw model
 Run on: August 10, 2004, 13:51:43 ; Search time 8672 Seconds
 (without alignments)
 12551.620 Million cell updates/sec

Title: US-09-875-228-1_COPY_5976_9620
 Perfect score: 3645
 Sequence: 1 ggccctcaataatgttaag.....ggaggaggctggactggc 3645

Scoring table: OLIGO_NUC
 Gappn 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 150

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 250 summaries

Database :

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EST:*
 1: em_estba:*
 2: em_esthum:*
 3: em_estin:*
 4: em_estmu:*
 5: em_estcov:*
 6: em_estpl:*
 7: em_estro:*
 8: em_htc:*
 9: gb_est1:*
 10: gb_est2:*
 11: gb_htc:*
 12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estcom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rdt:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %	Query No.	Score	Match Length	DB ID	Description
No matches found					

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OM nucleic - nucleic search, using sw mode!

Run on: August 10, 2004, 13:51:43 ; Search time 13686 Seconds
(without alignments)
11543.574 Million cell updates/sec

Title: US-09-875-228-1_COPY_5976_9620

Perfect score: 3645

Sequence: 1 ggccctcaataatgtttaag.....ggasaggactgtgactggc 3645

Scoring table: Oligo_NUC
Gapop=60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 150

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

Database : GenEmbl:
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_on: *
5: gb_ov: *
6: gb_dat: *
7: gb_dn: *
8: gb_dl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_ur: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_dat: *
24: em_ph: *
25: em_pl: *
26: em_lo: *
27: em_sts: *
28: em_ut: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_nus: *
34: em_htg_pln: *
35: em_htg_rod: *
36: em_htg_ran: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query	Match	Length	DB	ID	Description
	1	3645	100.0	12047	6	AR078691		AR078691 Sequence
	2	3645	100.0	12047	6	AR66428		AR66428 Sequence
	3	3645	100.0	12047	6	AX259151		AX259151 Sequence
	4	3645	100.0	12047	6	AX262356		AX262356 Sequence
	5	3645	100.0	12047	6	BD195482		BD195482 Adenoviru
	6	3645	100.0	12047	6	BD224259		BD224259 Adenoviru
	7	3645	100.0	12282	9	AF113169		Homo sapi
	8	2750	75.4	40458	9	AC011523		Homo sapi
	c	9	2750	75.4	2	AC027602		Homo sapi
	10	2750	75.4	21346	2	AF243527		Homo sapi
	11	1626	44.6	34560	9	AC037199		Homo sapi
	12	1369	37.6	5002	9	AF174646		Homo sapi
	13	1172	32.2	1172	6	AR078696		Sequence
	14	993	27.2	1172	6	AR078697		Sequence
	15	993	27.2	1172	6	AR078698		Sequence
	16	171	4.7	203	6	AX113818		Sequence

ALIGNMENTS

RESULT	1	LOCUS	AR078691	DEFINITION	Sequence 1 from patent US 5964371.	ACCESSION	AR078691	VERSION	AR078691.1	KEYWORDS
		SOURCE	Unknown.	ORGANISM	Unknown.	UNCLASSIFIED				
		REFERENCE	1 (bases 1 to 12047)	AUTHORS	McCabe,R.Paul.					
		TITLE	Disposable reservoir for evaporative coolers	JOURNAL	Patent: US 5964371,A 11-DEC-1999;	FEATURES	LocationQualifiers			
					1. 12047		1 /organism="unknown"			
						/mol_type="unassigned DNA"				
		ORIGIN								
		Query	GGCCCTCAATATTGTTAAGATGGAAATGTGTCRAAGTGGAAACTA	Match	100.0%	Score	3645,	DB	6	Length 12047;
		Best Local	GGCCCTCAATATTGTTAAGATGGAAATGTGTCRAAGTGGAAACTA	Similarity	100.0%	Pred. No.	0;			
		Matches	3645;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps 0;
Qy	1	Db	5976	Db	6036	Db	6036	Db	6036	Db
			CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA		CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA		CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA		CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA	
			61	Qy	61	Qy	61	Qy	61	Qy
			CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA		CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA		CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA		CTGCCCCAGAGATTCTCTGAGTTCTAGGTGAAATGTGTCAAAGTGAATGTTGAACTA	
			6096	Db	6096	Db	6096	Db	6096	Db
			CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGTTGGCT		CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGCT		CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGCT		CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGCT	
			6095	Qy	6095	Qy	6095	Qy	6095	Qy
			CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGCT		CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGCT		CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGCT		CTTCAGCTTAATGTTGAGGACATATTGACATGTTGCGACTGTTGTTGGCT	
			6156	Db	6156	Db	6156	Db	6156	Db
			CTTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG		CTTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG		CTTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG		CTTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG	
			6215	Qy	6215	Qy	6215	Qy	6215	Qy
			TCTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG		TCTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG		TCTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG		TCTGAAATCTGCTTCTGAGCATCTAGATCTGAGCTGTTGCTTCTGAGCATCTG	
			6225	Db	6225	Db	6225	Db	6225	Db

Qy	301	ATTATCTTGTAGGACATCTCCAGTCGGTTCTGCCCTCTGGCTCTAGGGCTGAGTCGTAGT	360	Db	7356	GTGACTCTATGTGCTAACATGGTAAAGAGATTAGCATGGCTTAG 7415
Db	6276	ATTATCTTGTAGGACATCTCCAGTCGGTTCTGCCCTCTGGCTCTAGGGCTGAGTCGTAGT	6335	Qy	1441	CACTCACAGATGCTCATCPAATCCTCACACATGGCTACAGGGGGCAGCTACTAGGCCCT 1500
Qy	361	CAGTACCCGGTCTGCAATTCACTTATAAGTGCTATACATGGCTATCTTGGCTCTAGGGCTGAGTCGTAGT	420	Db	7416	CACTCACAGATGCTCATCPAATCCTCACACATGGCTAAAGGGGGCTAGGCTACTAGGCCCT 7475
Db	6336	CAGTACCCGGTCTGCAATTCACTTATAAGTGCTATACATGGCTATCTTGGCTCTAGGGCTGAGTCGTAGT	6395	Qy	1501	ATTGCAAGAGGAAGGACTCTGGATAAGAGGGGGTACCCAATAGGTCAGAGTCATCT 1560
Qy	4211	CAACCAAACACCGATAAACATTAGAACCTTCCCACCTCCCTAACCTGGCTAGTCGTAGTAA	480	Db	7476	ATTGCAAGAGGAAGGACTCTGGATAAGAGGGGGTACCCAATAGGTCAGAGTCATCT 7535
Db	6396	CAACCAAACACCGATAAACATTAGAACCTTCCCACCTCCCTAACCTGGCTAGTCGTAGTAA	6455	Qy	1561	GGATGGAAAGGGGCTCAGGGACCATGGCTAGTCATGGTCAAGAAATTATGGCTGG 1620
Qy	4811	ACCTAGGATTCTCTGTTTAATGGTTCATATGAAATTTCAGCCTGATCAACTTACAT	540	Db	7536	GGATGGAAAGGGGCTCAGGGACCATGGCTAGTCATGGTCAAGAAATTATGGCTGG 7595
Db	6456	ACCTAGGATTCTCTGTTTAATGGTTCATATGAAATTTCAGCCTGATCACTTACAT	6515	Qy	1621	ATGTCMCTGCCCTGACCTTCTGGAAAGGGGGTACCTTCTGGCTACGCCCTATCTCAGATCTGACT 1680
Qy	5411	TCCCTCTACCGTTANTCAGCCTAACCCACCCTAACCTGGTAAATTCCTGGATT	600	Db	7596	ATGTCMCTGCCCTGACCTTCTGGAAAGGGGGTACCTTCTGGCTACGCCCTATCTCAGATCTGACT 7655
Db	6516	TCCCTCTACCGTTANTCAGCCTAACCCACCCTAACCTGGTAAATTCCTGGATT	6575	Qy	1681	TTGACGTTATCTCAGACTCTCTATGATACCCGACCTCATATACTCTCTGTGNC 1740
Qy	6011	CTACCTATATGGTAAATCTGGCTTCGGCAAGTCTGGTCAATTAACTACGTGATT	660	Db	7656	TTGACGTTATCTCAGACTCTCTATGATACCCGACCTCATATACTCTCTGTGNC 7715
Db	6576	CTACCTATATGGTAAATCTGGCTTCGGCAAGTCTGGTCAATTAACTACGTGATT	6635	Qy	1741	TCTCCCTTCTCTCAGCTTCTCAGCTTACTGCCACTCTCCAGCTCAGCTGGCCAGGTG 1800
Qy	6661	CATTCTTACTTAAAGGAAATAAGGCTCCCTGAGACTTCAAGGTTCTCAGA	720	Db	7716	TCCTCCCTTCTCTCAGCTTACTGCCACTCTCCAGCTCAGCTGGCCAGGTG 7775
Db	6636	CATTCTTACTTAAAGGAAATAAGGCTCCCTGAGACTTCAAGGTTCTCAGA	6695	Qy	1801	TAGGCCAGTACCTAACTCTTGGAGAGAACTTAAATGTTGATCTCCATCAGGGAGAAA 1860
Qy	7211	TGGCCCTTACCTCTGACATCAATTGAGATTCAATGAGATTTCAGGTTCACTCTCAGGT	780	Db	7776	TAGGCCAGTACCTAACTCTTGGAGAGAACTTAAATGTTGATCTCCATCAGGGAGAAA 7835
Db	6696	TGGCCCTTACCTCTGACATCAATTGAGATTTCAGGTTCACTCTCAGGT	6755	Qy	1861	AAAAAAAGAACTCTGAAAGAGCTGACATTTCAGGCTGCAAAACATAGCTAACCTG 1920
Qy	7811	TCA GTGATCTGGTAGGCCTCATATAACTCAATGAAACCTGTTATGCTCATGGCTATGG	840	Db	7836	AAAAAAAGAACTCTGAAAGAGCTGACATTTCAGGCTGCAAAACATAGCTAACCTG 7895
Db	6756	TCA GTGATCTGGTAGGCCTCATATAACTCAATGAAACCTGTTATGCTCATGGCTATGG	6815	Qy	1981	CCACACCTAAGGCAAGGATGAACCTTGTTCAGATTGTCATCTGGCCCAATT 2040
Qy	8411	TTTATTACAGCAAAAGAATAGAGATGAAATCTAGCAAGGGAAAGGTGCACTGGAA	900	Db	7956	CCACACCTAAGGCAAGGATGAACCTTGTTCAGTTGTCATCTGGCCCAATT 9015
Db	6816	TTTATTACAGCAAAAGAATAGAGATGAAATCTAGCAAGGGAAAGGTGCACTGGAA	6875	Qy	2041	CATAGGGATGATCAGGCAAGGATGTCATCTGGCCCAATTGGCTGGCAAGGTGAG 2100
Qy	9011	GACAGGGAGGCTCAAGGCAAGGATCTCTCTCCAGTCAGGTTCTCAGTGGCAAA	960	Db	8016	CATAGGGATGATCAGGCAAGGATGTCATCTGGCCCAATTGGCTGGCAAGGTGAG 8075
Db	6877	GACAGGGAGGCTCAAGGCAAGGATCTCTCTCCAGTCAGGTTCTCAGTGGCAAA	6935	Qy	2101	CAACCTAGGTTGAGATCTCACTTAAAGAGACTACTGCAATTGTCAGTCTGGCT 2160
Qy	9611	GCAGPATCTCTCCATCATATGATGTTGTTGATAATTCTGTTGATTCGGCAATAGGAAAC	1020	Db	8076	CAACCTAGGTTGAGATCTCACTTAAAGAGACTACTGCAATTGTCAGTCTGGCT 8135
Db	6936	GCAGPATCTCTCCATCATATGATGTTGTTGATAATTCTGTTGCACTCTCATG	6995	Qy	2161	TGTATCTGAGGAGATATTATCTTAAATTGGTTGAAGGAGACTACTGCGGAA 2220
Qy	10211	TCAACTGAGCCTGATTATGAGATGTTGTTGACAAGACATGTCGACACCTTATGG	1080	Db	8136	TGTATCTGAGGAGATATTATCTTAAATTGGTTGAAGGAGACTACTGCGGAA 8195
Db	6996	TCAACTGAGCCTGATTATGAGATGTTGTTGACAAGACATGTCGACACCTTATGG	7055	Qy	2221	CATATGTTATTATGTCCTGAAAGGAACTCTGTCAGGTTAACCTTCACTCC 2280
Qy	10811	CTGAACCTTGTAGTACTTGGCCCTTCAAGCTCACTGTTGAGCTGATGGCTTACCCAACTT	1140	Db	8196	CATATGTTATTATGTCCTGAAAGGAACTCTGTCAGGTTAACCTTCACTCC 8255
Db	7056	CTGAACCTTGTAGTACTTGGCCCTTCAAGCTCACTGTTGAGCTGATGGCTTACCCAACTT	7115	Qy	2281	ATTATCAAGGCAAGTAACTGAAACCTCTGTCAGGCAATCTGAAAGGCTACT 2340
Qy	11411	GTCACCATAAATCACATTGTTAGACTTCACTGGCCAAAGCTCCGGTGTAAACACAG	1200	Db	8256	ATTATCAAGGCAAGTAACTGAAACCTCTGTCAGGCAATCTGAAAGGCTACT 8315
Db	7116	GTCACCATAAATCACATTGTTAGACTTCACTGGCCAAAGCTCCGGTGTAAACACAG	7175	Qy	2341	GCTGTCACAAATATGTTGAAAGGTCAGGAAACGTTTATGCTCTTCTGCT 2400
Qy	12011	AAAGGCCTGGCCTTGGCAAGGAACTCTCCAGTCAGCTTACAGGGTT	1320	Db	8316	GCTGTCACAAATATGTTGAAAGGTCAGGAAACGTTTATGCTCTTCTGCT 8375
Db	7236	AAAGGCCTGGCCTTGGCAAGGAACTCTCCAGTCAGCTTACAGGGTT	7295	Qy	2401	CAGAGACACAGAAACATAAGGAAACCATGGAAAATGTCCTCCAAACACTCTTCACTCC 2460
Qy	13211	ATTGTGAGGATCAAATGIGCTCATGTGTGATGACACGGCAATGTCCTGGTGTGAA	1380	Db	8376	CAGAGACACAGAAACATAAGGAAACCATGGAAAATGTCCTCCAAACACTCTTCACTCC 8435
Db	7296	ATTGTGAGGATCAAATGIGCTCATGTGTGATGACACGGCAATGTCCTGGTGTGAA	7355	Qy	2461	AGAGGCCTGGCCTTGGCAAGGAACTCTCCAGTCAGCTTACATGTTGCTCTTCACTCC 2520
Qy	13811	GTGACTCTATGTGTCACATGGCTAAAGAAGGTTAGGCTATGGCTAAAGAAGT	1440			

Db	8436 AGAGCCCTCCACTCTGTCAGAACAGTCTAAACATCCATTAACATGGTCTACCA	8495	Qy	3601 GCCAGACGGGCCATGACGGGGCATGGGTGGAGGGCTGGACTGGC	3645
Qy	2521 CATCTGCCTTACCGTCAACCAGATTCTAGTCCAGTCTCCACATGGTCTACCA	2580	Db	9576 GCCAGAGGGCATGGGTGGAGGGCTGGACTGGC	9620
Db	8496 CATCTGCCTTACCGTCAACCAGATTCTAGTCCACAGATTCTAGTCCAGTGG	8555			
Qy	2581 GTGCCCAACTCCAACTGAGGAGTGTCAAGAATTCCGAGGGACATGGTGG	2640		RESULT 2	
Db	8556 GTGCCCAACTCCAACTGAGGAGTGTCAAGAATTCCGAGGGACATGGTGG	8615	Db	AR266428 LOCUS Sequence 11 from patent US 6495130.	PAT 10-APR-2003
Cy	2641 GGATCAGAACATTCTGGCTGAGTCAGAGGGGCCAACATCTTGGTCCGAAGGG	2700	Db	AR266428 DEFINITION AR266428	
Db	8616 GGATCAGAACATTCTGGCTGAGTCAGAGGGGCCAACATCTTGGTCCGAAGGG	8675	Cy	AR266428 KEYWORD SOURCE Unknown.	
Qy	2701 AAGAGGCTGGAGGTAAATGTTGTTCTGAGCTCTGAACCTTAATCC	2760	Db	AR266428 ORGANISM Unknown.	
Db	8676 AAGAGGCTGGAGGTAAATGTTGTTCTGAGCTCTGAACCTTAATCC	8735		REFERENCE 1 (bases 1 to 12047)	
Qy	2761 CCAAGGGAGGAGCTGGTCCAGTCTGGGAAATGGCTGAG	2820		AUTHORS Henderson, D.R. and Yu, D.C.	
Db	8736 CCAAGGGAGGAGCTGGTCCAGTCTGGGAAATGGCTGAG	8795		TITLE Target cell-specific adenoviral vectors containing E3 and methods of use thereof	
Qy	2821 AGGTCTAAGATCCCTATCTGGAAAGGGCTGAAATTGTGAGCTGTC	2880		JOURNAL Patent : US 6495130-A 11 17-DBC-2002;	
Db	8796 AGGTCTAAGATCCCTATCTGGAAAGGGCTGAAATTGTGAGCTGTC	8855		FEATURES Location,Qualifiers	
Qy	2881 AGGGGTTGTTAGCTTGAGCTCCCTGGGGAAAGGAACTGGAACTT	2940		source 1 ..12047 /organism "unknown" /mol_type="genomic DNA"	
Db	8856 AGGGGTTGTTAGCTTGAGCTCCCTGGGGAAAGGAACTGGAACTT	8915		ORIGIN	
Qy	2941 GGCTCAGGGTTGGTAGGTTGGTGAAGGTAATGGATCCAGGGACT	3000		Query Match Score 3645; Best Local Similarity 100.0%; Pred. No. 0; Matches 3645; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;	
Db	8916 GGCTCAGGGTTGGTAGGTTGGTGAAGGTAATGGATCCAGGGACT	8975	Qy	1 GGCCTCAATTATTTGTTAAAGGTGTAATGGTCCAAAGTGGAAATGGTGGAACTA	60
Qy	3001 GAGAGTTGCCATGTTGATCTTCCATCTACTCTTACTCCACTGAGGT	3060	Db	5976 GGCCTCAATTATTTGTTAAAGGTGTAATGGTCCAAAGTGGAAATGGTGGAACTA	6035
Db	8976 GAGACTTGGCCATGTTGATCTTCCATCTACTCCACTGAGGT	9035	Qy	61 CTGTCAGAGGATTCTGGTGGTCAAGCTGGTGGAAATATAGAACCTGGAGCTGGCT	120
Qy	3061 TACTCTTGTAGTTCCACAGAGTGGCTGGCAGTATAATCTGCAATGTC	3120	Db	6036 CTGTCAGAGGATTCTGGTGGTCAAGCTGGAAATATAGAACCTGGAGCTGGCT	6095
Db	9036 TACTCTTGTAGTTCCACAGAGTGGCTGGCAGTATAATCTGCAATGTC	9095	Qy	121 CTTCAACCTGAAATCAGGAAATCAGGAAATGGGCTGAACTTGAACTTGGG	180
Qy	3121 CGAGGCCCTGGCATCATCACTATCATTCAGCATTCAGCTGGCTATGGGG	3180	Db	6096 CTTCAACCTGAAATCAGGAAATGGGCTGAACTTGAACTTGGCTGGCTGG	6155
Db	9096 CGAGGCCCTGGCATCATCACTATCATTCAGCATTCAGCTGGCTATGGGG	9155	Qy	181 GTTGGCTTCCGAGCACATATTGACATGTTGCTGGCTGATTGGTTGGATTTC	240
Qy	3181 CGCATATGACTCATGACTCTAGTCTGGGACTATCCCTGGAGCCCTCTGGTCAGTCCC	3240	Db	6156 GTTGGCTTCCGAGCACATATTGACATGTTGCTGGCTGATTGGTTGGATTTC	6215
Db	9156 CGCATATGACTCATGACTCTAGTCTGGGACTATCCCTGGAGCCCTCTGGTCAGTCCC	9215	Qy	241 TCTGAATCCATTATGTTGCTGGCATCTAGATCTGAATTCGATTCAGAATTCT	300
Qy	3241 CCATGGAGCTGGGAGCTGGTCCCTGGGCTGGTGGCTGGCCAGGCCGG	3300	Db	6216 TCTGAATCCATTATGTTGCTGGCATCTAGATCTGAATTCGATTCAGAATTCT	6275
Db	9216 CCATGGAGCTGGGAGCTGGTCCCTGGGCTGGTGGCTGGCCAGGCCGG	9275	Qy	301 ATTATCTGAGTGGACATCTCCAGCTGGCTGGCTGGCTGGCTGGCTGG	360
Qy	3301 CCTGGTGGCATTAAGAGCTCAACACAGAAACAGGACTGAANGGTGAGAA	3360	Db	6276 ATTATCTGAGTGGACATCTCCAGCTGGCTGGCTGGCTGGCTGG	6335
Db	9276 CCTGGTGGCATTAAGAGCTCAACACAGAAACAGGACTGAANGGTGAGAA	9335	Qy	361 CAGTGACCCGGTCTGGCATTTCACCTTCATATAGTGCTGGCTGGCTGGCTGG	420
Qy	3361 TGGCATATGTCGTGTCCTGAAATCTAAGGACTCTGGGTGGCAAGGGCCT	3420	Db	6336 CAGTGACCCGGTCTGGCATTTCACCTTCATATAGTGCTGGCTGGCTGG	6395
Db	9336 TGGCATATGTCGTGTCCTGAAATCTAAGGACTCTGGGTGGCAAGGGCCT	9395	Qy	421 CAACCAAACACGGATAAACCATGAAACCTTCCCACCTTCCTAGTGCATGTTIA	480
Qy	3421 GAACTTACGGTTGCCCAAGTCAGTCATCTCCAACTGAACTGGCA	3480	Db	6396 CAACCAAACACGGATAAACCATGAAACCTTCCCACCTTCCTAGTGCATGTTIA	6455
Db	9396 GAACTTACGGTTGCCCAAGTCAGTCATCTCCAACTGAACTGGCA	9455	Qy	481 ACCTAGGATTCTGGTTAATGGTTCATATGAAATATTGCTGTCACCTTACAT	540
Qy	3481 CTGTGCCAGCATGAGCTTCACTCTGGTACACATCTGGTCAAGGGACT	3540	Db	6456 ACCTAGGATTCTGGTTAATGGTTCATATGAAATATTGCTGTCACCTTACAT	6515
Db	9456 CTGTGCCAGCATGAGCTTCACTCTGGTACACATCTGGTCAAGGGACT	9515	Qy	541 TCCTCTACGGTTATCTAACCCACCTTAAATGCTTCCGATATTCGCAATGTTAA	600
Qy	3541 ATGAAACACATGGCTGGCAGGAGGGGGTGAAGCCATGGACTCTGGTCA	3600	Db	6516 TCCTCTACGGTTATCTAACCCACCTTAAATGCTTCCGATATTCGCAATGTTAA	6575
Db	9516 ATGAAACACATGGCTGGCAGGAGGGGGTGAAGCCATGGACTCTGGTCA	9575	Qy	601 CTACCTATATGTTAATCTGGTAATCTGGCTGGCTGGCTGGCTGGCTGG	660

6576	CTACCTATATACTGTTAATCTGGCTTTCAGGATTCTAGGCATTAAACATGATTAA 6635	Qy	1741	TCTCCCTTCCTCAGTCTACTGCCACTCTCCAGTCTCATCTCGCTTCAAGGTG	1800
661	CATTCTTTACTTAAGTGGAAATAAGAATCCTGAGGTTCTGAGTTCTCAAGA 720	Db	7716	TCTCCCTTCCTCAGTCTACTGCCACTCTCCAGTCTCATCTCGCTTCAAGGTG	7775
6636	CATTCTTTACTTAAGTGGAAATAAGAATCCTGAGGTTCTGAGTTCTCAAGA 6695	Qy	1801	TAGCCAGTACTCTAATCTTCTGAGAAACTATTAATGTTATCTACAGGGAGAAA	1860
721	TGCCCCTTACTTCTGACATCAATTGAGATTTCAGGGAGTCGCCAAGATCATCCTCAGGT 780	Db	7776	TAGCCAGTACTCTAATGTTACGAGAACTATTAATGTTATCTACAGGGAGAAA	7835
6696	TGCCCCTTACTTCTGACATCAATTGAGATTTCAGGGAGTCGCCAAGATCATCCTCAGGT 6755	Qy	1861	AAAAAAGAACCTCTGAAAGAGTGCAGACTTACGACTGAAACATACTAACTCTG	1920
781	TCACTGATTGCTGGTAGCCCTCATATACTCAATGAAAGCTGTATGCTATGG 840	Db	7836	AAAAAAGAACCTCTGAAAGAGTGCAGACTTACGACTGAAACATACTAACTCTG	7895
6756	TCACTGATTGCTGGTAGCCCTCATATACTCAATGAAAGCTGTATGCTATGG 6815	Qy	1921	CGAGTTTGTTGTTGAGAACTCTAGAGACTCTGGCTAGAGCAAAGATTTTATAC	1980
841	TTTATTACGCAAAGAAATAGAGATGAAATCTAGCAAGGGAAAGAGTTCATGGCAA 900	Db	7896	CGAGTTTGTTGTTGAGAACTCTAGAGACTCTGGCTAGAGCAAAGATTTTATAC	7955
6816	TTTATTACGCAAAGAAATAGAGATGAAATCTAGCAAGGGAAAGAGTTCATGGCAA 6875	Qy	1981	CCACAGCTAAAGGCCAGCATGAACCTTGTGTTCAATTGTTGCTACCTTGCCTCCATT	2040
901	GAAAGGGAGGTCOCAAGTCAGAGATCCTGTTCTCCAGGGTTCTGTCATGAA 960	Db	7956	CCACAGCTAAAGGCCAGCATGAACCTTGTGTTCAATTGTTGCTACCTTGCCTCCATT	8015
6876	GAAAGGGAGGTCOCAAGTCAGAGATCCTGTTCTCCAGGGAAAGAGTTCATGAA 6935	Qy	2041	CATACTGGATGATGAGGACTGAGGAGTCAAGGTTGAGAACAGGGTTTGTGAAAGGTGAG	2100
961	GCACATCTTCCTCCATACATGATGTTGTTAAATTCAGTGTGATTCAGGAA 1020	Db	8016	CATACTGGATGATGAGGACTGAGGAGTCAAGGTTGAGAACAGGGTTTGTGAAAGGTGAG	8075
6936	GGAGTATCTCTCCATACATGATGTTGTTAAATTCAGTGTGATTCAGGAA 6995	Qy	2101	CAACCTAGGCTTAAAGAAATCCCTCAATCTTAAAGAAGGTACTAGCAACCTACTCTGAGCTT	2160
1021	TCAACTGACCCCTGATTATATGGAGCTGGTTGACAGACATGTCACCCCTCATG 1080	Db	8076	CAACCTAGGCTTAAAGAAATCCCTCAATCTTAAAGAAGGTACTAGCAACCTACTCTGAGCTT	8135
202	TCAACTGACCCCTGATTATATGGAGCTGGTTGACAGACATGTCACCCCTCATG 7055	Qy	2161	TGATATCTACGGAGATAATTATCTTAAATGGTTAAAGAGAACCTACTCTGAGCTT	2220
Db	8116	DB	8116	TGATATCTACGGAGATAATTATCTTAAATGGTTAAAGAGAACCTACTCTGAGCTT	8195
7056	CTGAACTTAACTGACTTACCTGCCCTCCAGAGCTTACAGCTGTTAAACCAAT 1140	Qy	2221	CATATGTTATTATGTTCTGAGACTAAACAATCTGCTGTAAPAGACGTTAACTCTT	2280
Db	8256	DB	8256	CATATGTTATTATGTTCTGAGACTAAACAATCTGCTGTAAPAGACGTTAACTCTT	8255
1141	GTCACCATAAATCACATTAGCTTAACTAACAGTGTGAAACTCCGGTAAACAG 1200	Qy	2341	GCTGTCACAAATATGCTGAAAGATGTCAGGAAAGTCAGTGTGAAATTCGCTTGCT	2400
7116	GTCACCATAAATCACATTAGCTTAACTAACAGTGTGAAACTCCGGTAAACAG 7175	Db	8316	GCTGTCACAAATATGCTGAAAGATGTCAGGAAAGTCAGTGTGAAATTCGCTTGCT	8375
1201	GCACTCTAAACAGCAGGATTTCAGAGCTTAGAGTCAGCTCCCGAGGTGAATG 1260	Qy	2401	CAGAAGACACAGAAACATAGAAACCATGAAACCTCTGTCAGCTTACCC	2460
7176	GCACTCTAAACAGCAGGATTTCAGAGCTTAGAGTCAGCTCCCGAGGTGAATG 7235	Db	8376	CAGAAGACACAGAAACATAGAAACCATGAAACCTCTGTCAGCTTACCC	8435
1261	AAAAGACCTGGCTCTTGGCAACAGGAAACTCTTCAGTGTGAACTGGTT 1320	Qy	2461	AGAGCTTCCTCACTCTGTCAGGAGCTCTGTCAGTGTGAACTCTGTCAGCTTACCC	2520
7236	AAAAGACCTGGCTCTTGGCAACAGGAAACTCTTCAGTGTGAACTGGTT 7295	Db	8436	AGAGCTTCCTCACTCTGTCAGGAGCTCTGTCAGTGTGAACTCTGTCAGCTTACCC	8495
1321	ATTTGGAGGATCAAATGGTCATGTCAGTGTGCTCTGGAGA 1380	Qy	2521	CATCTGGCTTACCGTGCCTAAACAAAGTCTGTCAGTGTGAACTCTGTCAGCTTACCC	2580
7296	ATTTGGAGGATCAAATGGTCATGTCAGTGTGCTCTGGAGA 7355	Db	8496	CATCTGGCTTACCGTGCCTAAACAAAGTCTGTCAGTGTGAACTCTGTCAGCTTACCC	8555
1381	GTCAGCTTCAATGGTCATGTCAGTGTGCTCTGGAGA 1440	Qy	2641	GGATCAGAAGCTCTGGCTTACGGGAGCTACTCTGTCAGTGTGAACTCTGTCAGCTTACCC	8675
7356	GTCAGCTTCAATGGTCATGTCAGTGTGCTCTGGAGA 7415	Db	8616	GGATCAGAAGCTCTGGCTTACGGGAGCTACTCTGTCAGTGTGAACTCTGTCAGCTTACCC	8735
1441	CACTCAAGATGTCATCAATCTCACTGTCAGTGTGCTCTGGAGA 1500	Qy	2761	GGAGGCCACTGGCAACCCGAAATAAGGGACTCTGTCAGAATTGGGAGCATGGTGGTG	2640
7416	CACTCAAGATGTCATCAATCTCACTGTCAGTGTGCTCTGGAGA 7475	Qy	2701	AAGAGCTGGTGGAGGTGAACTGGGGAGCAATGGGGAGCATGGTGGTG	8795
1501	ATTTGACAGAGGAAGGACTGTGTTGATAAGGGGGTGCACAAATGGTGTAGTCATCT 1560	Db	8556	GTGCCCACTGGCAACCCGAAATAAGGGAGCATGGTGGTG	8615
7476	ATTTGACAGAGGAAGGACTGTGTTGATAAGGGGGTGCACAAATGGTGTAGTCATCT 7535	Qy	2641	GGATCAGAAGCTCTGGCTTACGGGAGCTACTCTGTCAGTGTGAACTCTGTCAGCTTACCC	2700
1561	GGATCCAAGGGGCTCCAGGAGCCTATGTTGAGAGAAATTATGGCTG 1620	Db	8676	AAGAGGGCTGGAGGAGCTGGTAAGGTCTCCAGGTAAGCTGGAAATGGCTGCTAG	2820
7536	GGATCCAAGGGGCTCCAGGAGCCTATGTTGAGAGAAATTATGGCTG 7595	Qy	2761	CCAGGGAGGAGCTGGTAAGGTCTCCAGGTAAGCTGGAAATGGCTGCTAG	8736
1621	ATGGCTCTCCTCCGGGAAAGGGGGTGCACATTTCCTGAGCTATGGTGTAGTCATCT 1680	Db	7596	ATGGCTCTCCTCCGGGAAAGGGGGTGCACATTTCCTGAGCTATGGTGTAGTCATCT	7655
1681	TGAGGGTTACTCTGAGCTTACGAGGACCTATGTTGAGAGAAATTATGGCTG 1740	Qy	2736	TGAGGGTTACTCTGAGCTTACGAGGACCTATGTTGAGAGAAATTATGGCTG	8795
7656	TGAGGGTTACTCTGAGCTTACGAGGACCTATGTTGAGAGAAATTATGGCTG 7715	Db	Db	TGAGGGTTACTCTGAGCTTACGAGGACCTATGTTGAGAGAAATTATGGCTG	7715

6876 GCAAGGAGGAGTCCAGTGAGATTCCTCGTGTGGTCATGGAA 6935
 961 CGATATCTTCCATACAAAGATGTTGATAATTCTAGTGTGGCATCGGGAAC 1020
 6936 CGATATCTTCCATACAAAGATGTTGATAATTCTAGTGTGGCATCGGGAAC 6995
 1021 TCAACTGACCTGATTAATTGGACCTGGTGCACAACTTCATGG 1080
 6996 TCAACTGACCTGATTAATTGGACCTGGTGCACAACTTCATGG 7055
 1081 CTGAACTTCTAGTACTTACATGTTAGCTTACAGCTGATAGCTGAACTTACACAT 1140
 7056 CTGAACTTCTAGTACTTACATGTTAGCTTACAGCTGATAGCTGAACTTACACAT 7115
 1141 GTCACCATTAATCACAATGTTAGACTTACAGCTGATAGCTGAACTTACACAG 1200
 7116 GTCACCATTAATCACAATGTTAGACTTACAGCTGATAGCTGAACTTACACAG 7175
 1201 GCACTTAACAGCGAGGATTTCAAAGTTAGATACTCCAGAGCTGAATGTC 1260
 7176 GCACTTAACAGCGAGGATTTCAAAGTTAGATACTCCAGAGCTGAATGTC 7235
 1261 AAAGACCTGGCTCTTGGCAAAAGGAAATCTTACCGCACACTCTCCCTCACAGGGTT 1320
 7236 AAAGACCTGGCTCTTGGCAAAAGGAAATCTTACCGCACACTCTCCCTCACAGGGTT 7295
 1321 ATTGTGAGGATCAAATGTTGCTCATGTGTGTGACATGTCTGGCTGGAGA 1380
 7296 ATTGTGAGGATCAAATGTTGCTCATGTGTGTGACATGTCTGGCTGGCTGGAGA 7355
 1381 GTGACTCTATGTTGCTAACTGTTGAGGACTTATAGGATGGCTTTCG 1440
 7356 GTGACTCTATGTTGCTAACTGTTGAGGACTTATAGGATGGCTTTCG 7415
 1441 CACTCAAGAAGCTCATCTAACTCTCAAGAACATGCTCAAGGGGGCAATACTAGGCC 1500
 7416 CACTCAAGAAGCTCATCTAACTCTCAACACATGCTCAAGGGGGCAACTAGGCC 7475
 1501 ATTTGACAGAGCAAAGGACTCTGGATAAAAGGGGCTGACCAATAGGTAGACATCT 1560
 7476 ATTTGACAGAGCAAAGGACTCTGGATAAAAGGGGCTGACCAATAGGTAGACATCT 7535
 1561 GGATGCAAGGGGCTCAAGGAGGACCATGTTAGACATTGCTGAGAAAATTATGGCTCG 1620
 7536 GGATGCAAGGGGCTCAAGGAGGACCATGTTAGACATTGCTGAGAAAATTATGGCTCG 7595
 1621 ATGTCTCTGCCCGGCAAGGGGATGCACTTCTCTGACCCCTPATCTAGATCTGACT 1680
 7596 ATGTCTCTGCCCGGAAAGGGGATGCACTTCTCTGACCCCTPATCTAGATCTGACT 7655
 1681 TTGAGGTATCTCAAGCTCTCTCATATACTCTGAGATAAGGGCCATCATGTC 1740
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 1741 TCTCCCCCTCCCTCACTTACTGCCCCACTTCCCAAGCTGGCAGCTG 1800
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 1921 CCAGTTTGTGCTGGTAGAACTCATGAGAACTCTGGTCAAGGGAAAGATTTTAAAC 1980
 7896 CCAGTTTGTGCTGGTAGAACTCATGAGAACTCTGGTCAAGGGAAAGATTTTAAAC 7955
 1981 CCACACTAAGGGAGCATGAACTTGTGTTCACATTGTTGACTTGGCCCCCAATT 2040
 8016 CATATGGATGATCAAGCTTACCTTCTGAGGAACTCTGGGATGAACTCTGGGAG 8075
 2041 CATATGGATGATCAAGCTTACCTTCTGAGGAACTCTGGGATGAACTCTGGGAG 2160
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 2161 TGTATCTGACGGAGATTATCTTAAATGGTGAACAGCTACTCTGGGAA 2220
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 2281 ATTATCTAAGGGAGTAACTCTGAACTCTGAAAGGCTGATACCATTCTGCAAGGGCTATCT 2340
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 2641 GGATCAGAACTCTGGCTTGGGCGCCAATCTCTGGTCTGAGAATCTGGCTGG 2700
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 2701 AAGAGGCTGGAGCTGTCATGGGCAATAAGGAGTCAGTCTGAGAATCTGGCTGG 2760
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 2761 CCAGGGGGAGACTGTTGCTGAGGAACTCTGGCTGGGATGGCTGAG 2820
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Qy	3121	CCGAGGCCCTGGGCATCATCCACTATCAGCATTCATTCAGGCTGGGTATGGCGAGGCCGG	31.80
Db	9096	CCGAGGCCCTGGGCATCATCCACTATCAGCATTCATTCAGGCTGGGTATGGCGAGGCCGG	91.55
Qy	3181	CCCCATCACTGCTCATGTAGCTCGACTATCCCTGCAGCGCCCTCTCCGCACGCCCCA	32.40
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Qy	3241	CCATGGAGCTGGACGTCGCTGCCCTGGTGGATGTCGCTGGCAGGGCGGG	33.00
Db	9216	CCATGGAGCTGGACGTCGCTGCCCTGGTGGATGTCGCTGGCAGGGCGGG	92.75
Qy	3301	CCTGGGTTCCGATAAAGATCTCTAGAACACCAGAACCTGAGAACAGGAGAGA	33.60
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Db	9336	TGGCCATATGTCGTCATGAAACTCAGGACTCTGGTGAGGGACAGAGCCT	93.95
Qy	3421	GAACTTACGGGTTGGCCAGTCACGTCTCCCTCAAGTACAGGA	34.80
Db	9396	GAACTTACGGGTTGGCCAGTCACGTCTCCCTCAAGTACAGGA	94.55
Qy	3481	CTGTGCCCAGCATGCTTCACTGTACACATCTTCAACGGACTTCAAGGACCTCTG	35.40
Db	9456	CTGTGCCCAGCATGCTTCACTGTACACATCTTCAACGGACTTCAAGGACCTCTG	95.15
Qy	3541	ATGAAACACATGGTGTGTCAGGAAAGGGCATGGACTCCCTGTGTCAGA	36.00
Db	9516	ATGAAACACATGGTGTGTCAGGAAAGGGCATGGACTCCCTGTGTCAGA	95.75
Qy	3601	GCCCCAGGGGCCATCACGGTGGGGAGGGGCTGGACTGGC	36.45
Db	9576	GCCCCAGGGGCCATCACGGTGGGGAGGGCTGGACTGGC	96.20
RESULT 4			
AX262356	AX262356	12047 bp	DNA
LOCUS	Sequence 11 from Patent WO0173093.		linear
DEFINITION	Sequence 11 from Patent WO0173093.		PAT 26-OCT-2001
ACCESSION	AX262356		
VERSION	AX262356.1		
KEYWORDS	GI:16511284		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
FEATURES	artificial sequences.		
source	1..12047		
organism	"synthetic construct"		
entry site			
JOURNAL	Patent: WO 0173093-A 11 04-OCT-2001;		
	Calydon, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..12047		
organism	"synthetic construct"		
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mol_type	"unassigned DNA"		
db_xref	"taxon:32610"		
note	"Human glandular kallikrein-TRE sequence"		
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y	3421	GAACCTAACGGTTCGGCGTCCCACTGTCTCCCAAGTCAAGTCTCCCAAGATACAGGC	3480	Qy	181	GTTGGCTTCGGGAGCACATATTGACATGTCAGTGTGGTGGTTGGTATTGCT 240
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b	3541	ATGAAACACATCGTTCATGTCAGGAAAGGGGTGAGGGCATGGACTCCTGTGGCAGA	3600	Qy	301	ATTATCTTGAGTAGGCAATCTCCAGTCTGCTGGTCTGGCTCTAGGCTGGAGTCGTAGT 360
y	9516	ATGAAACACATCGTTCATGTCAGGAAAGGGGTGAGGGCATGGACTCCTGTGGCAGA	9575	Db	6276	ATTATCTTGAGTAGGCAATCTCCAGTCTGCTGGTCTGGCTCTAGGCTGGAGTCGTAGT 6335
b	3601	GCCCCAGGGGCCATGACGGTGGGGAGGGAGGGCTGGACTGGC	3645	Qy	361	CAGTGAACCGGCTGGGATTCACCTCAATACATGGGATATCTTGTCAGTGTGGTT 420
y	9576	GCCCCAGGGGCCATGACGGTGGGGAGGGAGGGCTGGACTGGC	9620	Db	6336	CAGTGAACCGGCTGGGATTCACCTCAATACATGGGATATCTTGTCAGTGTGGTT 6395
b	ES3935			Qy	421	CAACCAAACACCGGATAAAACCTTGAACCTTCCACACTCCAGTGAATGTTAA 480
OCUS	D1193482	BD1193482	12047 bp DNA linear PAT 17-JUL-2003	Qy	481	ACCTAGGATTCTGTTAAATAGGTCATATGAAATAATTGACCTGATCCAACTTACAT 540
DEFINITION			Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same.	Db	6396	CAACCAAACACCGGATAAAACCTTGAACCTTCCACACTCCAGTGAATGTTAA 6455
ACCESSION	BD1193482	BD1193482		Qy	481	ACCTAGGATTCTGTTAAATAGGTCATATGAAATAATTGACCTGATCCAACTTACAT 540
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SOURCE	JP 2002514074-A/3.			Qy	541	TCCCTTACCGTTATCTACCCACCTTAAATGCAATTCCAAATATTCCTGGATT 600
ORGANISM	unidentified			Db	6516	TCCCTTACCGTTATCTACCCACCTTAAATGCAATTCCAAATATTCCTGGATT 6575
COMMENT	1. (bases 1 to 12047)			Qy	601	CTTACCPATAATGGTAAATCCGGCTTGCAGTTCTAGGTTACCTGGATT 660
EFFECTIVENESS	HENDERSON, D.R., YU, D.C. and LAMPARSKI, H.G.			Db	6576	CTTACCTTATATGGTAATCTGGCTTGGCGATTCTAGTGTGATTAA 6635
AUTHORS	Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same			Qy	661	CATTCTTACTTTAATGTCGAATAATAGAGTCCTCTSGAGGTTCAAGGTTCTCAAGA 720
TITLE	JP 2002514074-A 3 14-MAY-2002;			Db	6636	CATTCTTACTTTAATGTCGAATAATAGAGTCCTCTGGAGTTCTCAAGA 6695
JOURNAL	CALYDON INC			Qy	721	TGCCCCCTACTCTGACATCAATTGAGATTCAAGGGAGTCCTCTCAGGT 780
COMMENT	OS Unidentified			Db	6639	TGCCCCCTACTCTGACATCAATTGAGATTCAAGGGAGTCCTCTCAGGT 6755
PN	JP 2002514074-A/3			Qy	781	TGAGTATTGCTGGTGGAGCTTATGAGCTGTTATGCTCAGGCTATGG 840
PD	14-MAY-2002			Db	6756	TGAGTATTGCTGGTGGAGCTTATGAGCTGTTATGCTCAGGCTATGG 6815
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PR	03-MAR-1997	US 60/039763		Db	6816	TGATATTAGCAGAAAAGGATAGAGATGAAATCTAGCAGGAGGTGCTGGGCAA 6875
PR	03-MAR-1997	US 60/039762		Qy	901	GACAAGGAGAGCTCCAGTGCAGAGATCTGGTTCTCCAGTGTGTCATGGAA 960
04-AUG-1997	US 60/05523	03-MAR-1997		Db	6876	GACAAGGAGAGCTCCAGTGCAGAGATCTGGTTCTCCAGTGTGTCATGGAA 6935
R HENDERSON, DE CHAO YU, HENRY G LAMPARSKI	PC			Qy	961	GCGTATCTTCCATACATGATGTTGATATACTTCAATGCTGACATGGGAC 1020
C12N5/186, C12N5/10, A61K47/00, A61K47/48, C12N11/08	CC	Strandedness:		Db	6936	GCGTATCTTCCATACATGATGTTGATATACTTCAATGCTGACATGGGAC 6995
SINGLE;				Qy	1021	TGACTGAGCCCTGATATATGGGCTGGTGCAGACATGTCGACCTTCATGG 1080
CC	Topology: Linear;			Db	6996	TGACTGAGCCCTGATATATGGGCTGGTGCAGACATGTCGACCTTCATGG 7055
CC	Adenovirus vectors containing heterologous transcription	CC		Qy	1081	CTGAACTTCTAGTACTGCCCCTCCAGCTGCTGATAGTGTGCTAACCAACATT 1140
regulatory	elements and methods of using same			Db	7056	CTGAACTTCTAGTACTGCCCCTCCAGCTGCTGATAGTGTGCTAACCAACATT 7115
FT	Key	Location/Qualifiers		Qy	1141	GTCACCATAAATGACATGTTGAGCTTCAAGTGTGGCTAACCAACATT 1200
FT	source	1. .12047		Db	7116	GTCACCATAAATGACATGTTGAGCTTCAAGTGTGGCTAACCAACATT 1260
FT	/organism='Unidentified'.			Qy	1201	GCACTCTAAACAGCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
FEATURES	Location/Qualifiers	1. .12047		Db	7176	GCACTCTAAACAGCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
source	/organism='Unidentified'			Qy	1202	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
ORIGIN				Db	7177	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
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Matches 3645; Conservative				Qy	1204	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
1	GGCCTCAATAATGTTAGAGTGTAAATGTCGAAGATGAAATGTTGAGAAGTCA	60		Db	7179	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
5976	GGCCTCAATAATGTTAGAGTGTAAATGTCGAAGATGAAATGTTGAGAAGTCA	6035		Qy	1205	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
22	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 180			Db	7180	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
22	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 180			Qy	1206	CTGTCAGGATATTCTCAAAGCTTGAAGATGACCTCCAGGCTGATGC 7225
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Qy	3481	CTGGCCGCCATAGCTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC	3540	Db	6156	GTGCTTCCGAGCATATTGCACTGTGATTGGTTCAGTGGTGGTGGTGGTGGTGGTGGT	6215
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Qy	3541	ATGAAACCATGCTGTGTCAGAAGGGGTGAGGCTATGGCTATGGCTATGGCTATGGCTATGG	3610	Db	6216	TCTGAACTCTTATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC	6275
Db	9516	ATGAAACCATGCTGTGTCAGAAGGGGTGAGGCTATGGCTATGGCTATGGCTATGGCTATGG	9575	Qy	301	ATTATCTGACTGAGACATCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
Qy	3601	GCCCCAGGGGCCATGCGGTGGGGAGGGCTTGACTGGC	3645	Db	6276	ATTATCTGACTGAGACATCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6335
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Db				Db	6336	CAGTGAACCCGTCGACATTCACCTCATATACTGCTGCTGCTGCTGCTGCTGCTGCTG	6395
				Qy	421	CAACCAAACACGATAAACCTAGAACCTTCCCACCTGCTGCTGCTGCTGCTGCTGCTG	480
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RESULT 6							
BD224259		12047 bp DNA linear	PAT 17-JUL-2003				
LOCUS		Adenovirus vectors containing cell status-specific response elements and methods of use thereof.					
DEFINITION							
BD224259							
VERSION	BD224259.1	GT:33034029					
SOURCE	JP 200252063-A/5.						
ORGANISM	Homo sapiens (human)						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo. 1 (bases 1 to 12047)						
AUTHORS	Yu, D.C. and Henderson, D.R.						
TITLE	Adenovirus vectors containing cell status-specific response elements and methods of use thereof						
JOURNAL	Patent: JP 200252063-A 5 13-AUG-2002;						
COMMENT	CALYDON INC OS Homo sapiens (human) PN JP 200252063-A/5						
FT	PD 13-AUG-2002						
FT	PF 10-SEP-1999 JP 20000570347						
PR	PR 10-SEP-1998 US 60/0293791, 09-SEP-1999 US 09/392822 PI						
DE	DE CHAO TO, DANIEL R HENDERSON						
PC	PC C12N15/09 A61K48/00, A61P35/00, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10, C12N7/02//A61K35/76, C12N15/00, C12N5/00						
CC	CC Adenovirus vectors containing cell status-specific response elements and						
CC	CC methods of use thereof						
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Matches 3645; Conservative							
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Db	5976	GGCCCTCAATAATGGTAAGAGTGTAAATGTCAGTTCAGAGTGTGGAAATATGAACTGAGCTGGCTT	6035	Db	6996	TCAACTGAGCTTGTGATTATGGGCTCTGGTGCACAGCATGTCACCTCTGTTAGCTGCTGCTG	7055
Qy	61	CTGGCCCTGAGATCAGAGATTGTCAGAGTGTAAATGTCAGTTCAGAGTGTGGAAATATGAACTGAGCTGGCTT	120	Qy	1081	CTGAATTCTGAGCTTGTGATTAGCCCTCCAGAGCTTACAGTGTGATAGCTGCTGCTGCTGCTG	1140
Db	6036	CTGGCCCTGAGATCAGAGATTGTCAGAGTGTAAATGTCAGTTCAGAGTGTGGAAATATGAACTGAGCTGGCTT	6095	Db	7056	CTGAATTCTGAGCTTGTGATTAGCCCTCCAGAGCTTACAGTGTGATAGCTGCTGCTGCTGCTG	7115
Qy	121	CTTCAGGCTTAGATCAGAGATTGTCAGAGTGTAAATGTCAGTTCAGAGTGTGGAAATATGAACTGAGCTGGCTT	180	Qy	1141	GTCACCCATAATCACATGTTGAGATATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200
Db	6096	CTTCAGGCTTAGATCAGAGATTGTCAGAGTGTGGAAATATGAACTGAGCTGGCTT	6155	Db	7116	GTCACCCATAATCACATGTTGAGATATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	7175
Qy				Qy	1201	GCATCTAAACAGGAGGATTGTCAGAGTGTGGAAATATGAACTGAGCTGGCTT	1260
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				Qy	1261	AAAGACTGGCCTCTTGGCCAAAGGAAATCCCTACAGGCTACACTCTCCTTCAGAGCTT	1320

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Qy	1321	ATTGTGAGATCAATGTTGATGTTGAGACCACTGAAATTGCTCCAAACACTGTCACCCC	2460	Qy	2401	CAGAAGACACAGAACATAGAACCTGAAATTGCTCCAAACACTGTCACCCC	2460
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Qy	1441	CACTCAAGATGATCTCATCTAACTCTAACAACTGGCTAACGGCTGACTCTAGGCTC	1500	Qy	2521	CATCTGACTTCACTGCTGCTAACCAAGAGATTCCTAGTCCAGTTCCACCATGTTGGCA	2580
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Qy	1561	GGATGCAAGGGCTCOAGGAGGACCATGTTAGACATTTGCTGGAGAATTGGCTG	1620	Qy	2641	GGATGCAACTCTGGCTTGAATGGGAGGAGGGCCCATACTCTGGTCCAGAGGAGG	2700
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RESULT 7
LOCUS AF113169 12282 bp **DNA** linear PRI 05-MAY-1999
DEFINITION Homo sapiens glandular kallikrein enhancer region, complete sequence.
ACCESSION AF113169
VERSION AF113169_1
KEYWORDS GI:4164598
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiridae; Homo.
REFERENCE 1 (bases 1 to 12282)
AUTHORS Yu,D.C., Sakamoto,G.T. and Henderson,D.R.
TITLE Identification of the transcriptional regulatory sequences of human kallikrein 2 and their use in the construction of calydon virus 764, an attenuated replication competent adenovirus for prostate cancer therapy. *Cancer Res.* 59 (7), 1498-1504 (1999)
JOURNAL MEDLINE 99211477
PUBMED 10197620
FEATURES 2 (bases 1 to 12282)
AUTHORS Yu,D.C., Sakamoto,G.T. and Henderson,D.R.
TITLE Submitted (14-DEC-1998) Research, Calydon Inc., 1324 Chesapeake Terrace, Sunnyvale, CA 94089, USA
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ORIGIN

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Matches 3645; Conservative		

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DEFINITION Sequence 6 from Patent: US 5964371-A 6 12-OCT-1999;
ACCESSION AR078696.1 GI:10005442
KEYWORDS Location/Qualifiers
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1172)
AUTHORS McCabe, R., Paul.
TITLE Disposable reservoir for evaporative coolers
JOURNAL Patent: US 5964371-A 6 12-OCT-1999;
FEATURES source
Organism="unknown"
mol_type="unassigned DNA"

ORIGIN
Query Match 32.2%; Score 1172; DB 6; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0;
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Qy 1285 GAAATCTTACCGACACCTCCCTACAGGTTAATGGAGATCAAATGGGTCAAT 1344
Db 61 GAAATCTTACCGACACCTCCCTACAGGTTAATGGAGATCAAATGGGTCAAT 120
Qy 1345 GTGTGTAGAGCACCGACACATGTCGGTGGAGGTGACTCTATGTCGTAACATT 1404

Query Match Score: 171; DB: 6; Length: 203;
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ORIGIN

RESULT 16 AX113818 AX113818 203 bp DNA linear PAT 01-MAY-2001
 DEFINITION Sequence 64 from Patent WO0127256.
 ACCESSION AX113818
 VERSION AX113818.1 GI:113939984
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1. Wu, L., Carey, M. F., and Belldegrun, A. S.
 TITLE Chimeric transcriptional regulatory element and methods for
 prostate-targeted gene expression
 PATENT: WO 0127256-A 64 19-APR-2001
 JOURNAL The Regents of the University of California System (US)
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RESULT 17 AX113818 AX113818 203 bp DNA linear PAT 01-MAY-2001
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ORIGIN

Query completed: August 11, 2004, 01:15:47
 Job time : 13695 secs

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